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Mon Jun 26 09:10:26 2000

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AS2460 Sequence 4
AR009152 Sequence
M73260 Mastadenovi
J01917 Adenovirus
S82508 9E4: Orf2.
AF108105 Human aden
X51800 Adenovirus
L19443 Human aden
AD34817 Adenovirus
L19443 Human aden
AD026117 Porcine a
L43363 Mastadenovi
AF03132 Porcine a
L43363 Lanine aden
V07760 Canine aden
V07760 Canine aden
V07760 Canine aden
AF030154 Bowine aden
AF030154 Bowine aden
AF030154 Bowine aden
AF03154 Homo sapi
AC016797 Homo sapi
AC016797 Homo sapi
AC01638 Homo sapi
AC01638 Homo sapi
AC01838 Homo sapi
AC01847 Homo sapi
AC01859 Homo sapi
AC01850 Mesailes vir
X1656 Mesailes vir
AB012948 Mesailes vir
AB012949 Mesailes vir
AB012949 Mesailes vir
AB012949 Mesailes vir
AC016746 Homo sapi
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AC135905
AC006760
MEAPHOSPRA
X16567
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AB023583
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AF083334
ACO14231
AL136360
MMHC438N12
ACO1838
ACO07847
ACO11777
ACO22389
HS1732
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ABO12948
ABO12949
ACO16946
ACO10746
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AR009152
ADRCOMPGEN
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ADRCG
APROB
AF12CGA
ADERE4
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Match Length DB
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4.1 153442
4.0 123937
4.0 155083
4.0 180009
4.0 234131
3.9 2041
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.8 1654
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gb_htg11:
gb_htg12:
gb_htg13:
gb_htg13:
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1 atgactacgtccgcgttcc.....atgactctaccccatgtag 885
                                                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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em_hum4:
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RESULT 1 A52460/c LOCUS A52460 3189 bp DNA ACCESSION A52460 A52460 A52460 BETUILLY A52460 A52	Ouery Match Best Local Similarity 100.0%; Score 885; DB 5; Length 3189; Matches 885; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 atgactacgtccggcqttccatttggcatgacactacgaccaacacgatctcggttgtct 60 1 1328 Argacracgcactccgtrccarraggcargaccacacacacacacactcggttgtct 60 2	181 1148 241 1028 301 1028 421 t 421 t 421 t 848 T 788 A 788 A 788 A 601 gf	1

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Nucleotide sequence at the junction between the coding region the adenovirus 2 hexon messenger RNA and its leader sequence Proc. Natl. Acad. Sci. U.S.A. 75 (12), 5822-5826 (1978)
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Studies of low molecular weight RNA from cells infected
adenovirus 2. I. The sequences at the 3' end of VA-RNA I
J. Biol. Chem. 252 (24), 9032-9042 (1977)
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Studies of low molecular weight RNA from cells infected
adenovirus 2. II. Heterogeneity at the 5' end of VA-RNA
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Jornvall, H., Ohlsson, H. and Philipson, L.
An acctylated N-terminus of adenovirus type 2 hexon p.
Blochem. Blochys. Res. Commun. 56 (2), 304-310 (1974)
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Akusjarvi,G. and Pettersson,U.
Sequence analysis of adenovirus DNA. I. Nucleotide se
virology 91 (2), 477-480 (1978)
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Ohe, K. and Weissman, S.M.
The nucleotide sequence of a low molecular from cells infected with adenovirus 2 7. Biol. Chem. 246 (22), 6991-7009 (1971)
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Zain, B.S. and Roberts, R.J.
Characterization and sequence analysis
the hybrid virus Ad2+ND
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Precise localization and nucleotide sequence of the two mouse
mitochondrial rRNA genes and three immediately adjacent novel
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Anderson, C.W. and Lewis, J.B.
Anderson, C.W. and Lewis, J.B.
Anino-terminal sequence of adenovirus type 2 proteins: hexon, fiber, component IX, and early protein lB-15K, 10, 27-41 (1980)
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Predicted structure of two adenovirus tumor antigens
Proc. Natl. Acad. Sci. U.S.A. 77 (7), 3778-3782 (1980)
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Buttner,W. and Veres-Molnar,Z.
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fragalization of the 3'-terminal end of the
fragment-specific early mRNA of adenovirus
FEBS Lett. 122 (2), 317-321 (1980)
Nucleotide sequence of the EcoRI D fragment Nucleic Acids Res. 8 (10), 2173-2192 (1980) 81053687
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22 (bases M., Padmanabhan, R.V. and Padmanabhan, R. Shinagawa, M., Padmanabhan, R.V. and Padmanabhan, R. Shinagawa, M., Padmanabhan, R.V. and Padmanabhan, R. San and the standard adenovirus type 2 DNA General (1980)
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                                                                                                          12 (bases 6039 to 6079; 7101 to 7172; 9634 to 9723; 18802 to 18861) Akusjarvi,G. and Pettersson,U. Sequence analysis of adenovirus DNA: complete nucleotide sequence of the spliced 5' noncoding region of adenovirus 2 hexon messenger
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Perricaudet, M., Akusjarvi, G., Virtanen, A. and Pettersson, U.

Structure of two spliced mRNAs from the transforming region of

Structure of two adenoviruses

Nature 281 (5733), 694-696 (1979)
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Gallbert, F., Herisse, J. and Courtols, G.
Nucleotide sequence of the EcoRI-F fragment of adenovirus
Gene 6 (1), 1-22 (1979)
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Zain,B.S. and Roberts,R.J.
Sequences from the beginning of the fiber
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Herisse,J., Courtois,G. and Galibert,F.
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/db_xref="G1:1699393"
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37.2%; Score 328.8; DB 16; Length 3119;
Best Local Similarity 63.1%; Pred. No. 9.3e-85;
Matches 526; Conservative 0; Mismatches 302; Indels 6;
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Human adenovirus type 9

Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

1 (bases 1 to 3119)

Javier,R. and Shenk,T.

Mammary tumors induced by human adenovirus type 9: a role for the Breast Cancer Res. Treat. 39 (1), 57-67 (1996)
$82508 3119 bp DNA VRL 03-DEC-1996 9E4: orf2. .orf7 [adenovirus type 9, Genomic, 6 genes, 3119 nt]. $82508.1 G1:1699390
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/Tote="E4"
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Human adenovirus type 17
Human adenovirus type 17
Yuness; ABDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
1 (bases 1 to 35100)
Chillon,M., Bosch,A., Zabner,J., Law,L., Armentano,D., Welsh,M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group D adenoviruses infect primary central nervous system cells more efficiently than those from group C J. virol. 73 (3), 2837-2840 (1999) 99139039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2601 ceriecrereceacecaccaccacacacacrearecreaaecrereces
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             1941 CAATCCAGCTCGCCCATCATCCATATCGCAGGGCCCGTTTACCACGATCTGATGAG 2000
                                                                                                                                             646 ttgaacaatattgtggtgctgtgctgcagttactgtgctgatttaagtgagatcagggtg
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                                                                                                                                                                                                                            2001 GAAACCAGGGCTTCACTGACTGAACAACATCCCCTGTTGCCCGGATTGTGATCATGCAGAT
                                                                                                                                                                                                                                                                                                                166 atgcacaacgtgagttacgtgcgaggtcttccctgcagtgtgggatttacgctgattcag
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AF108105
AF108105.1 GI:4416335
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INSTNVQSNLDRLYTDVREXVAQREREKNEGLGSIVALNAFLATOPANVPRQDDDYIN
FISALRLAWYVEVPOSEVYOSEDVIFOOTSROGLOTVULSOAFRULRGLWGVAAPVGDB
FISALRLAWSKLLLILLIAPPTDSGSVNRNSYLGHLLTIRRAIGAAVVDEGTI
SVSSLLTPNSRLLLLILAPPTDSGSVNRNSYLGHLLTIRRAIGAAVVDGGTFOEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MQQAPDPAIRAALQSQPSGLASDDWEAAMQRIMALTTRNPESFR
                                                                                                                                                                                                                                                                                                                                                                                           VDNDRYPSHVASFVLAWTRAFVSEWSEFLYBEDRGTPLODRPIKSVYODTDSLEVTER
GHRLMETRGKKRIKKRIGGKLYFDPEQPELTWLVECETVCAHCGADAFAPESVFLAPKL
YALQSLLCPACGRSSKGKLRAKGHAAEALNYELMVNCYLADAQGEDRARFSTSRMSLK
                                                                                                                                                                                                                                                                                                                                                                                                                          RTLASAQPGAHPETVTETTLTRTLRPWKDMTLAALDAHRLVPYSRSRPNPRNEEVCWI
EMP"
2 (bases 1 to 35100)
Armentano,D. PhD and Souza,D.W.
Direct Submission
Submitted Diversion
New York Ave., Framinham, MA 01701-9322, USA
Location/Qualifiers
                                                                                             /organism-"Human adenovirus type 17"
/db_xref-"taxon:46922"
complement(4991. 8266)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="terminal protein"
/protein_id="AAD20326.1"
/db_xref="GI:4416342"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAD20321.1"
/db_xref="GI:4416337"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(8311. .10161)
                                                                                                                                                       /product-"DNA polymerase
                                                                                                                                                               /protein_id="AAD20327.1"
/db_xref="G1:4416343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="L155K"
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                                                                                                                                             /codon_start=1
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585

645

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complete genome; core protein; DNA polymerase; DNA-binding protein; endoprotease; fiber protein; hexon protein; large T-antigen; maturation protein; minor core protein; penton protein; peripentonal hexon-associated protein; promoter; repeat region; small t-antigen; transcriptional activation.

Human adenovirus type 12

Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                      32931 idiaidicadidiccididiccccdciaccidgacriggraagagcrcagargc 32872
                                                                                                                                                     32871 GGGTACGAGCGCTGGATCCTGCATTGCCACTGTTCATCCCCTGCTCGCTGCAGTGTCGG 32812
                                                                                                                                                                                                                         32571 CTGAATAACATGGTGATTATGTGCTGCACTTACTGTGAGAACATGGCAGAGATCAGGATG 32512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32451 GAGACTIGIGAICCCGAICCCATIGCAGCAGCGCACCAAGCCCCGGCGGCAGAGACIG 32392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              species specificity of 12 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sprengel, J., Schmitz, B., Heuss-Neitzel, D., Zock, C. and Doerfler, Nucleotide sequence of human adenovirus type 12 DNA: comparative functional analysis
                                                                                                                                                                                                                                                                                  tgtatgcacgtgtgcctgtgttgtgccaacattgatatcatgacgagcatgatgatccat
                                                                                                                       ggttacgagtcctggggctctccactgtcattgttccagtcccggttccctgcagtgtata
                                                                                                                                                                                                    gccggcgggcaggttttggccagctggtttaggatggtggtggatggcgccatgtttaat
                                                                                                                                                                                                                                                                                                          atgtccagcgtgtttatgaggggtcgccacttaatctacctgcgcttgtggtatgatggc
                                                                                                                                                                                                                                                                                                                                                                                                                                              cacgigggitcigiggicccgccatgagcitiggatacagggccttgcactgigggatt
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Direct Submission
Submitted (21-JUN-1993) J. Sprengel, Institute of Gen
Virology, Weyertal 121, 50931 Cologne 41, FRG f
3 (Dases 1 to 34125)
Cock, C. Iselt, A. and Doerfler, W.
A unique mitigator sequence determines the species sp
the major late promoter in adenovirus type 12 DNA
93124560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AT12CGA 34125 bp DNA AT12CGA Adenovirus type 12 DNA, complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virol. 68 (1), 379-389 (1994)
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ENGELAPLYTRYTLYDNKSADIASLNYCNDHSNFLTTVVQNNDFTPRAASTQTINFDE
RSRWGGDLRTILHTNMPNYESVETSFKRARVYARKHDGVFATDLISTDLLEVFRF
RTD.BEGRRSETWITILHTNMPNYENFTSFKRARVYARKHDGVFATDLISTDLLEVFRF
FTL.BEGRRSETWITILHTNYCOVENGRGVLESDIGWFDSRNFKLGWDPVTKL
PALLDPRYKLESKKKLEBARLENAARANGPRGDSSSVSREPERSABKELVIEPIKGDDT
RRSYNLLEGTWOTLYFGWYLLSTTRDPENGYOSWTLLTFPVYTGABCOVTSPLEDLMQ
DPVTFRSTQOVSNY PVVGAELMPFRAKSFYNDLAVTSGLIRSTSTLTHVVRIEPDLMQ
LCRPPAPTITTVSENVPALTDHGTLERSKSTRGVYTDARRACETVA
ATPSAALDMTARNMEPSMYAANRPFINKLMDYLHRAASMNSDYFTNAILNPHWLPPPG
FYTGEYDMPDPNDGFLWDDVDSAVFSPTLQKRQEAVRTPASEGAVGRSPFPSLGSLHS
LPGSVNSGRVSRPRLLGEDEYLNDSLLQPPRVKNAMANNGIESLVDKLNRWKYYAQDH
REPAPAPRRONHDRORGLVWDDEDSADDSSVLDLGGSGGVNPISKILQPKLGRRMF"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAD20323.1"
/db_xref="G1:4416339"
/tanslation="MEDINFASLAPRHGTRPFMGTWNEIGTSQLNGAFNWSSVWSGL
KNFGSTLRTYCONKAMNSSTGGLLERKLKDQNFQGKVVDGLASGINGVVDIANQAVQRE
INSRLDPRPPTVVEMEDATLPPPRGEKRPRDDAEETILQVDEPPSYERAVKAGMPTTR
IIAPLATGVWRRATLDLPPPPTPAPPRAAPVVQPPFVATAVRRVPARRQAQNWQSTLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAD20324.1"
/db_xref="G1:4416340"
/translation="MSGSSERELASIVRDLGCGPTFWAPTTORFPGFLAGDKLACAIV
NTAGRETGYTWLAGGWNPREATCTMFDPFGFSDRRLKQIYSFEYEARLRRSAVASSP
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SPQVLPTLRRNQEELYRFLARHSPYFRSHRAAIEHATAFDKNKQLRVSQ"
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SANKLSLKVGHGLKILDDKSAGGLKDLIGKLVVLTGKGIGTENLQNTDGSSRGTGISV
RARBGLIFDNDGYLVAWNPKYDTRTLMTTPDTSPNCRIDKEKDSKLTLVLTRGGSQIL
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SEAYKNAVEFWPNLVAYPKPTJGSKKYARDIVYGNI YLGGLAYQPVV I KVTFNEEADS
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RLTVNIMSRPRIETYYWQELQDEPQRGDMHLQYKYSFEQLKTHWLEPWEDMECAIKAF
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ITFINVRFAGDKFKGIMFEANTCLVLHGVYFLNFSNICVESNNKVSARGCTFYGCWKG
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/note-"ElA; transcription activation; darly protein,
alternative splicing; crossref SWISS-PROT:EIA_ADE12,
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/note="crossref Ad12 EPD07152"
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/note="crossref SWISS-PROT:E1BS_ADE12, P04492"
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protein_id="CAA51878.1"
db_xref="GI:313363"
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protein_id="CAA51879.1"
db_xref="G1.313364"
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Sapporo Igaku Zasahi 52, 253-267 (1983)
10 (Bases 20966 to 22966)
110 (Bases 20966 to 22966)
120 Structure and Schalk, P.M., Speijer, J.G. and Sussenbach, J.S. Structure and function of adenovirus DNA binding protein: comparison of the amino acid sequences of the Ad5 and Ad12 proteins derived from the nucleotide sequence of the corresponding genes viricity 128 (1), 140-153 (1983)
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Juttermann,R., Weyer,U. and Doerfler,W.

Juttermann,R., Weyer,U. and Doerfler,W.

Jeffort of adenovirus type 12 replication in hamster cells: absence of transcription of viral virus-associated and L1 RNAs

J. Virol. 63 (8), 3535-3540 (1989)
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Engler, J.A. and van Bree, M.P.
The nucleotide sequence of the gene encoding protein IVa2 in human
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Shinagawa, M. and Padmanabhan, R.
Shinagawa, M. and Padmanabhan, R.
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Proc. Natl. Acad. Sci. U.S.A. 77 (7), 3831-3835 (1980)
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Shibata,H., Zheng,J.H., Koikeda,S., Masamune,Y. and Nakanishi,Y.
Cis- and trans-acting factors for transcription of the adenovirus
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Kimura, T., Sawada, Y., Shinawawa, M., Shimizu, Y., Shiroki, K.,
Shimolo, H., Sugisaki, H., Takanami, M., Uemizu, Y. and Fujinaga, K.
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adenovirus type 12 DNA: structure and gene organization, and
comparison with those of adenovirus type 5 DNA
Nucleic Acids Res. 9 (23), 6571-6589 (1981)
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                                Shu,L.M., Hong,J.S., Wei,Y.F. and Engler,J.A.
Nucleotide sequence of the genes encoded in early region 2b of human adenovirus type 12
Gene 46 (2-3), 187-195 (1986)
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Sugisaki, H., Sugimoto, K., Takanami, M., Shiroki, K., Saito, I.,
Shimojo, H., Sawada, Y., Uemizu, Y., Desugi, S. and Fujinaga, K.
Structure and gene organization in the transformed Hind III-G
fragment of Adiz
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Tolun,A., Alestrom,P. and Pettersson,U.
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Gene 19 (1), 71-80 (1982)
                  (bases 4831 to 10470)
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100 FEB-1990) Hogenkamp T., Institute of Molecular 10.00043 (cancer Research), University of Essex, Hufelandstr 55, se < v00043> for overlapping sequence.
Location/Qualifiers
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Human adenovirus type 12.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
1 (bases 1 to 3498).
Hogenkamp.T. and Esche,H.
Nucleotide sequence of the right 10% of adenovirus type 12 DNA encoding the entire region E4.
Nucleotide Acids Res 18 (10), 3065-3066 (1990).
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/protein_id="CAB57853.1"
/db_xref="G1:6018361"
/translation="MRIPOTPPPYSRDTAACIAWLGLAHASCVDTLRFIKHHDLKITPEARYILASLREWLYFAFLTERQRCKQKGRGAITSGRTWFCFFKYEDARKSVYYDAAR
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QSGSIANIEEFERDNARALLEFIEIRAVALLEAVVEHLENRLQFDLAVIFHQHSGGDRCH
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Submitted (06-FEB-1990) Hogenkamp T., Institute of Molecular
Biology (Cancer Research), University of Essex, Hufelandstr 55,
4300 Essen 1, F R G
See <VO0043> for overlapping sequence.
Location/Qualifiers
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Davison, A.J., Telford, E.A., Wetson, M.S., McBride, K. and Mautner, V.
The DNA sequence of adenovirus type 40
The DNA sequence of 4), 1308-1316 (1993)
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                                                                                                                         fastidious adenovirus types 40 and 41 Gene 58, 109-126 (1987)
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Tooglood.C.I., Murall,R., Burnett,R.M. and Hay,R.T.
Trooglood.C.I., Murall,R.) becomes sequence, predicted structure
relationship to other adenovirus hexons
J. Gen. Virol. 70, 3203-3214 (1989)
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Vos, H.L., van der Lee, F.M., Reemst, A.M., van Loon, A.E. and Sussenbach, J.S.
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van Loon,A.E., Ligtenberg,M., Reemst,A.M., Sussenbach,J.S.
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(idd.A.H. and Erasmus,M.J.
equence characterization of the adenovirus 40 fiber gene
irology 172, 134-144 (1989)
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Characterization of Adenovirus type 40 El region
Virology 165, 95-102 (1988)
Nucleotide sequence of the ademovirus type 40 inverted repeat: Close relation to that of ademovirus type 5 Virology 156, 414-416 (1987) 87122182
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/organism="Human adenovirus ty/solate="Dugan"
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/tissue_lib="ATCC VR-931"
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/standard_name="EIA 249R"
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/note="for ElA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIIGIGCCACIAIAAAIGIIGAAGIIACICAAIIAIIACAIGGICAIGAGCGGIGGCIIA 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  725 caaggogocttatgctgogggoggtgogaatcatcgctgaggagaccactgccatgttgt 784
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                                                                                                                                                                                                                                                                                                                                     1597 CTTCGGAAAATTCTTTATGGCCTGAGTGTAAAGTCTGACTTTACATAATGTGAGG 1538
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Ishino,M., Sawada,Y., Yaegashi,I., Demura,M. and Fujinaga,K.
                                                                                                                    68 ctccgtacagtagggatcgtctacctcctttgagacagaaacccgcgctac---catac 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        attectgcaggacggagcggcggcagcagtttattcgcgcgctgctgcagcaccacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 ccagctggtttaggatggtggtggtggcgccatgtttaatcagaggtttatatggtacc
                                                                                                                                                                                                                                                                                                      tgcgaggtcttccctgcagtgtgggatttacgctgattcaggaatgggttgttccctggg
                                                                                                                                                                                                                 125 tggaggatcatccgctgctgcccgaatgtaacactttgacaatgcacaacgtgagttacg
                                  Length 3498;
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADRGENOME 34214 bp DNA URBHuman adenovirus type 40, complete genome.
                                    DB 16;
                                  Score 273.8; DB 16;
Pred. No. 8.9e-69;
0; Mismatches 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gecetatectgatgeacgattatga 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGCAATTTTATTTGGAGATTATAA 853
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                                         Query Match
Best Local Similarity 59.6%;
Matches 480; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
ADRGENOME/C
LOCUS
POETNITION PACCESSION I
VERSION SCURCE
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ORGANISM
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AUTHORS
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AKVALREDTIYTIKKYVNIRKCAYULGNGAVVRFOTCDRVAFNCANGSLGFGLIGANG
VTFMNVRFVVEGFNGTVFASTTQLTLHGVPFONCGGICVDSWGRYSARGCTFVACWKG
VGFNKSQMSVKKCVFERCIMAMYVEGQARIRHNAGSDNYCFLLLKGTASYKHNICG
GGHSQLLTCADGNCQALRYFYSHPRRPWPVFEHNMLMRCTVHLGARRGMFSPYGSN
FCHTXVLMTDAFSRVWMNGYPDLTMBLFKVYRYDESKVRCRPGEGGANHIRLYPATL
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                                                                                                                                                                                                                                                                                                                          | Orin Carlow Control 
                                                                                   /translation="MERPNSSYAGIYSGLHGNGSVENLAREBEGLRLLAGAASARFGS
SAGRGGGGEPEGRPGPFNGIVTEPDPEEGISSGGRGGINGORGTRRKMENBGEDFLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     // Translation="MSGFTEGNAVSFEGGVFSPYLTTRLPSWAGVRQNVVGSNVDGRP
VAPANSTILTYATIGSSVDTAAAAAASAAASTARGWAADFGLYNQLAASRLREEDALS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32565 CCTTTTGTAGTATTGCAGGAGTGGCCAATGTGGTGGGACATGATATTGTCTAAATGGGAA 32506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32505 AAGCAIGIGGAAAATITACAIGCGIGTITGTGTGTTGCGIGCGCACIAITAAIGITGAI 32446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 ctacctccttttgagacagaaaccggcgctaccatactggaggatcatccgctgctgccc 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gaatgtaacactttgacaatgcacaacgtgagttacgtgcgaggtcttccctgcagtgtg 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 ggatttacgctgattcaggaatgggttgttccctgggatatggttctaacgcgggaggag 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 34214;
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Best Local Similarity 54.0%; Pred. No. 1e-53;
Matches 455; Conservative 0; Mismatches 388; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <1719. .1938
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                                                                                                  /translation="mem.pdfftoneddmfggilleteryfdfpepseasemsihdle
DVEVDGFEEDANGEAVDGPISDAEGESESGSPEDTDFPHPLIAIPPHGIVRIPCRVS
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                                                                                                                                                                                                                                                                                                                                                                                                     /number=1
join(486. .927,1088. .1311)
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407. .>1407
note="ElA-ElB cotranscript"
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                                                                                                                                                                                        <486 .1011
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standard_name="EIA 249R"
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/product-"ElA 214R"
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boul.
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/note="Description: E1A; homologous to E1A 289R of human adenovirus 2 and 5; putative early genes transactivater, anduction of host cells DNA synthesis and activate p53 dependent apoptosis cascade"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                              1. .34094
/organism="Porcine adenovirus 3"
/db_xref="taxon:35265"
/note="drictine adenovirus 3 strain IAF is a high titer
/note="drivated from strain 6618 and adapted for cell
line PKA (pig kidney, porcine circovirus free)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32025 GIGAAAGIGIIGGGAAGCIICACCGIIAGGICACICAIGAGGAGCIIGGIGGAACCCCGG 31966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31965 AGACAGGGATTACTGCGGGGGTTGATGGAGCGGTACTGCCCGTTTACGTTGGCAGACTAC 31906
                                                                                                                                                                                                                                                                                                                                                                                                  32085 INGGANGAGCITICIGIGCGGIGCIGCCCCCGCGGACGCGGCGGCGCCTGCCAAGGCG 32026
                                                                                                                                                                                                                                                                                                            32145 TITITAGTTATGGAATTATGAATAATATGGTGGTGTTGGGCTGTACCTATTGTAAAAC 32086
                                 32385 GGGTCTCTTCAATGTAAGGCGGGGGGTGTAGTGTTAGCAAATTGGTTTAAAATGATGATT 32326
                                                                                                                                                                                                                                                                                                                                                                 747
                                                                                                                                                                                                                                                                                                                                                                                                                                         807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             808 eggeageagtttattegegegetgetgeageaceacegecetatectgatgeacgattat 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           porcine adenovirus serotype 3, complete genome porcine adenovirus serotype 3, complete genome upublished (1999)

2 (bases 1 to 34094)

Laroque, L., Malenfant,F., Massie,B. and Dea,S.
Linect Submission Submitted (14-APR-1999) to the DDBJ/EMBL/GenBank databases. Submitted (14-APR-1999) to the DDBJ/EMBL/GenBank databases. Laroque, INRS-Institut Armand-Fraappier, Biotechnology; 531 laroque, Location, Quebec HYN 423, Canada (Bemaliais, Laval, Quebec HYN 423, Canada (E-mailaidaniellarocque@videotron.ca, Tel:(450) 687 5010)
                                                                                                                                                                                                                                                                                                                                                                 ttaagtgagatcaggggtgcgctgtgtgcccggaggacaaggcgccttatgctgcgggcg
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388 ggttccctgcagtgtatagccggcgggcaggtttggccagctggtttaggatggtggtg
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/note="possible promoter region of ElA genes"
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porcine adenovirus 3 DNA, complète
AB026117.1 GI:4630864
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TATA_signal
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1461. 2069
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13661. - 15115
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RVVSISRREANDEELMFGLRRALAGGEGEDLEEEEEDLEEAEGGVRSPGTAA
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Naveavarrraarrssrmgttgdpvadvvaaveavarrrrstrrrrsapailgvr
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GSYASPTNIHGGGTRDDKVTPLYFTNNPATEAEALEENGLKPUVTLYSEDVDLKAPDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="49% homologous with protein IIIa of human adenovirus ad2 and ad5"
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CDS

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160 T. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 acaatgcacaacgtgagttacgtgcgaggtcttccctgcagtgtgggatttacgctgatt 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aatcagaggittatatggtaccgggaggtggtggtgaattacaacatgccaaaggaggtaatg 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31574 GACTATGCCAATTACATAGTGCTGGTGTGCCGGCGCTGCCACGAGCTGAGCGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 34094;
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                                                                                                                                                                                                                                                                                                                                                                                                                       7.3%; Score 65; DB 16; Le
45.2%; Pred. No. 4.9e-08;
tive 0; Mismatches 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      823 cgcgcgctgctgcagcaccaccgccctatcctgatgcacgattat
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Matches 319; Conserv
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VVQBRSMSLSEKVAAINYSYATLAKHYARKISTFYMRAVVKLLVLADDLGMYRNERLE
RVVSTSRRRELNDEELMFGLRRALAGEGEEDLEEEEBDLEEAEBEELERGGVRSPGTAA
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Rveeaggysaarahmsaaslagayegtvreevnfoktfinnnvrtlysrdeytmglwhl
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/traislation-"mssegeirayfbayfbyndsaydcmyroalaelrqoloelreyvb
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1829. .3253
                                                                                                                              /function="putative inhibitor of apoptosis by p53
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/gene="major late promoter (MLP)"
6009. .6015
/gene="major late promoter (MLP)"
complement(855. .>10396)
/function="essentiel for DNA replication"
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complement(5962, .5965)
                                                                                                                                                                                                                                   /product="ElB 474R"
                                                                                                                                                                                         dependent mechanism"
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4085. .4090
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SAVAARVLSELADVYFEGGESEDSGSAAGDSGSGGVFEMDPPEGDSNEEDI
vDGLPBPWLDSVLL"
/product="E1A"
/product="E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Larycque, D.

Direct Submission

Direct Submission

Submitted (GS-FEB-1999) Larocque D., INRS-Institut Armand-Frappier,
Institution/Qualifiers

/strain="IAR"
/strain="IAR"
/strain="IAR"
/strain="IAR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porcine adenovirus 3
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
1 (bases 1 to 34094)
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/db_xref="high titer clone derived from strain 6618 and /note="high titer clone derived from strain 6618 and adapted for cell line PKA (pig kidney, porcine circovirus
                                                                                                                                                                                                                                           AJ237815.
AJ237815.1 GI:4678602
100 kDa protein; 202R; 214R; 229R; 474R; 52 kDa protein; COOH
101 kDa protein; 202R; 214R; 229R; 474R; 52 kDa protein; COOH
102 kDa protein; Els; fiber protein; hexon; IIIa; penton protein;
103 proteinase; PTP; pVII; pVIII.
104 Porcine adenovirus 3.
                                                                                                                                                                        PAD237815 34094 bp DNA VRL 04-MAY-1999
Porcine adenovirus serotype 3 complete genome, strain IAF.
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/gene="EIA"
1461. .206.
/function="putative inhibitor of apoptosis (Bcl-2
homologue)"
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/rpt_type=TERMINAL
/49. .452
/gene="ElA"
/note="possible promoter region of ElA genes"
/49. .1291
/gene="ElA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Larocque, D., Malenfant, F., Massie, B. and Dea, S. porcine adenovirus serotype 3, complete genome unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 34094)
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/qene="E1A"
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ATVERGGESYLGFLSALRLLVSEVPOTEVFRGCPHTFLQAARNGSKTVNLNQAMENLR
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LHVDERTYQETISVSRALGDEDDAARLQATLNFFLTNRQRRLPAAYALTAEEERILRY
VQQAVSLYLMQDGATATGALDEASRNLEPSFYAAHRDFINRLMDYFHRAAAVAPNYFM
                                                                                                                                                                                 NAVLMRWLPEGGFFTGVYDPPEQDEGEBRPWDAFDSDEEGRLMLRSAASSEPSSSFT
PLPLTEEPPSRPSTPALSRVPSRASSLLSLASIGKREGGDSLAYSPATPTYGSRWGSR
RSSLASGADGLEWDALLAPPRDVNEHPGAAAGRRRRASRSSLEEDIDAISSRLETWRT
RAQEMGLPVASFSRRHOPRPGALEDDEEEEDWRQDRFFRFEAPEENPFRHIAPKGL"
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STYNAMFPHDVYLAPGCAIDFTFSRLNNLLGIRKRYPYQEGFNLTYEDLAGGNPALL
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VQRYIVTDARRRVCPYVYKSLGVYDFNYEDROGILLRPPESTITSISENVPSLTDHGTLPLRNSIPG
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INLDERSKRØGGEFKSILTTNIPNVTQYMFSNSFRVRLMSARDKETNAPIYEWFILTLD
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AQTNMTKDWFLVQMLAHYNIGYQGYHLPEGYRDRTYSFLRNFEPMCRQVFDYANHKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLEVPTINOFNSSGEVSBARTAGNREGHEYPANNTISFLIGEDAVOPTANHUDE
WRIPESENEMSMOTLTDLGONLLYANSAHALDMTFEVDAMDEPTLLYVLFEVEDRTL
HOPHRGVIEAVYLRTPFSAGNATT"
21990. . 22544
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/function="major core protein; packaging of viral DNA"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32048 ACGTIGCALCCGGIGGGGCCGTGCGCAACAGCCGGGCCGCGGTATGTTITGTTCCCTGT 31989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31988 TIGGAGALTGIGGICCCCIGGCGCTACAICCITICCCAICAAGAAIGGATTTCCIGCAG 31929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 acaatgcacaacgtgagttacgtgcgaggtcttccctgcagtgtgggatttacgctgatt 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 aagigtaigcacgigtgccigigitgigccaacaitgaiatacaigacgagcaigaigaic 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 4.9e-08;
0; Mismatches 380; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSRRLRKRISS"
11906. .21912
/function="major virion component"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="penton protein"
/protein_id="CAB41028.1"
/db_xref="GI:4678611"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /prote1n_1d="CAB41029.1"
/db_xref="G1:4678612"
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/protein_id="CAB41030.1"
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Matches 319; Conserv
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31751 AATCGCATCTTCTGGTGGTTCAGGGAGGGGGTGAACCTGCCCAGGGTGAGTCGCGTGATG 31692
                      31868 ---GGGCGCGAGCTGTGGAACTTTCATTGCCACTGTCTGAAAAGGTCCAGTCTGGAGTGC 31812
                                                                                          31811 CGCGCGGGCAGGTGTGTGCTCTCTTGTGCGCGAATCATCCGGGGCTGCGAGTAC 31752
                                                                                                                                                                                                                            31691 TACGTGGGCAGTGTGATGTTTGAGGGGCGCCCACCTGATGTAAAGATCATGTATGAC 31632
                                                                                                                                                                                                                                                                                                                                                                          31574 GACTATGCCAATACATAGTGCTGGTGTGCCGGCGCTGCCACGAGGTGAGCCGGGGG 31515
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                                                                                                                                                                                                                                                                                                                                                                                                                                         11514 GCTCGGCCCTACCGCTTGCGGCACTGGCTGAAGCTGGCGGAGGCCATCGGG 31455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31454 GCGCAGCGGCGGGGAAGCAGCAGTTCACGGAGGGGGAATGGTGGTCCCGGCAGAGG 31395
catggttacgagtcctgggctctccactgtcattgttccagtcccggttccctgcagtgt 402
                                                                               462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reddy S., Idamakanti N., Derbyshire J.B., Nagy E., "Characterization of the early region 4 of porcine adenovirus type 3";
                                                                403 atagccggcgggcaggttttggccagctggtttaggatggtggtggatgggccatgttt
                                                                                                                                     aatcagaggtttatatggtaccgggaggtggtgaattacaacatgccaaaaggaggtaatg
                                                                                                                                                                                                                                                                                                           31631 Tergarcre---AAGCretrecgCATGTTCCACTGGGGGGAGGTCATCTACTGTGACGGG
                                                                                                                                                                                                                                                                          583 ggccacgtgggttctgtggtccccgccatgagctttggatacagcgccttgcactgtggg
                                                                                                                                                                                                                                                                                                                                              643 attitigaacaatatigiggigcigitgcigcagitacigigcigatitaagigagatcagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porcine adenovirus 3
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31394 GACGCGGAGCGGGAGGAGGAGGCCAGAGGCCCTCCAGGAGTGT 31350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          823 cgcgcgctgctgcagcaccaccgccctatcctgatgcacgattat 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:35265"
/sequenced_mol="DNA"
/organism="Pocrine adenovirus 3"
/sub_strain="6618"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JAN-1996 (Rel. 46, Created)
04-JAN-1996 (Rel. 46, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA; VRL; 3028
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/codon_start=1
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/gene="L1"
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ORGANISM
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ACCESSION
VERSION
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                                                                                                                                                           REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2636 GCGCAGCGGCGGGGGAGGAAGCAGCTTCACGGAGGGGGAGTGGTGGTCCCGGCAGAGG 2695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2399 TACGIGGGCAGIGIGAIGITICGAGGCGCCCACCIGAIGIACAIAAAGAICAIGIAIGAC 2458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2459 IGIGAICIG---AAGCIGIIGCGCAIGIICCACIGGGGGGAGGICAICIACIGIGACGGG 2515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2279 cececedecrecrestarcecrecrestececeresterresegestres
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                                                                                                                           /note="homology to Human Adenovirus 34 kDa polypeptide;
19.8 kDA polypeptide; NCBI 91: 1146152"
/protein_id="CAB24462.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2161 TACAGCCTGTGTGGGGGGTTGGAGCTGGAGCAGATATGTTTCAGCCCGGAGACGCTGTGC 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2221 GGGCGCGAC--GCTGTGGAACTTTCATTGCCACTGTCTGAAAAGGTCCAGTCTGGAGTGC 2278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2041 ACGINGCANCCGGNCGGGGCCGNGCGGCAACAGCCGGGCGGCGGGTANGINIGGNCCTGN 2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tttatgtccagcgtgtttatgagggtcgccacttaatctacctgcgcttgtggtatgat 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 atagccggcggcaggttttggccagctggtttaggatggtggtggatggcgccatgttt 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catggttacgagtcctgggctctccactgtcattgttccagtcccggttccctgcagtgt 402
                                                                                                                                                                                                                                                                                                                                                                                       Or 163 acaatgcacaacgtgagttacgtggagtcttccctgcagtgtgggatttacgctgatt 222
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aatcagaggtttatatggtaccgggaggtggtgaattacaacatgccaaaagaggtaatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggccacgtgggttctgtggtccccgccatgagctttggatacagcgccttgcactgtggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aagtgtatgcacgtgtgcctgtgttgtgccaacattgatatcatgacgagcatgatgatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 caggaatgggttgttccctgggatatggttctaacgcgggaggagcttgtaatcctgagg
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                                                                                                                                                                                                                                                                  XX.
SQ ... Sequence 3028 BP; 562 A; 789 C; 991 G; 686 T; 0 other;
                                                                                                                                                                                                                                                                                                                          Score 62.2; DB 31;
Pred. No. 2.6e-07;
0; Mismatches 383;
                                        'note="inverted terminal repeat"
                                                                                                                    /db_xref-"SPTREMBL:Q84211"
        /strain="PAV-3"
1. .144
                                                                                        297. .2788
codon_start=1
                                                                                                                                                                                                                                                                                                                            query Match 7.0%; 25-36st Local Similarity 45.0%; 25-36st Matches 317; Conservative
                                                                                                                                                                                                                                                   2903. .2909
                                                    repeat_region
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                                                         TATA_signal TATA_signal
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INLDERSRWGGEFKSILTTNIPNWTOYMENSREPRRILMSARDKETRAFTETTE
ENGESDIAV YDLANNBALVENTAVROGOVKEEDIGVKIDTRNFRLGYDPETKITLE
SYTNAR-HPDVVLAGEOCAIDFYSRLNNLLGIRKRYPYGEOFMLTTEDLAGGNIPALL
DLTTYDOENSSTIKPLKODSKGRSYHVGEDPEAGDTFTYTSBWILLYTGBLAGGNIPALL
AUTSGOLLOGATNITLYFRREPENGILLEPPSGTPSYTSBWILLYTGBPAGTGTAS
AVYSGOLLOGATNITLYFRREPENGILLEPPSGTPSYTSBWILLYTGBPAGTAS
VSGOLLOGATNITLYFRREPENGILLEPPSGTPSTTSSENVPSLIPHGTLPLRINSIPS
VQCYTYTDARRRUCPYVXKSLGVVTPNYLSSRTF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (07-AUG-1998) Veterinary Microbiology, Veterinary Infectious Disease Organization, 120 Veterinary Road, Saskatoon, Saskatchewan S7N 5E3, Canada On Jan 4, 1999 this sequence version replaced gi:1146142 gi:606653 gi:1146151.
                                                                                                                                                           Porcine adenovirus 3.

Porcine adenovirus 3

Porcine adenovirus 3

Viruses; daDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

Vibases 1 to 34034)

Reddy, P.S., Nagy, E. and Derbyshire, J.B.

Reddy, P.S., Nagy, E. and Derbyshire, J.B.

Sequence analysis of putative pVIII, E3 and fibre regions of porcine adenovirus type.

Porcine adenovirus type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reddy, P.S., Tuboly, T., Dennis, J.R., Derbyshire, J.B. and Nagy, E. Comparison of the inverted terminal repetition sequences from five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 34094)
Reddy, P.S., Idamakanti, N., Derbyshire, J.B. and Nagy, E.
Characterization of the early region 4 of porcine adenovirus type
Virus Genes 15 (1), 87-90 (1997)
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Reddy, P.S., Idamakanti, N., Song, J.Y., Lee, J.B., Hyun, B.H.,
Park, J.H., Cha, S.H., Bae, Y.T., Tikoo, S.K. and Babluk, L.A.
Nucleotide sequence and transcription map of porcine adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence and transcription map analysis of early region-1 of porcine adenovirus type 3 Virus Res. (1999) In press 6 (bases 1 to 34094)
   03-JAN-1999
VRL
Porcine adenovirus 3 strain 6618, complete genome.
AF083132 L43077 U10433 L43363
AF083132.1 GI:4092658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              porcine adenovirus serotypes
Virology 212 (1), 237-239 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 acaatgcacaacgtgagttacgtgcgaggtcttccctgcagtgtgggatttacgctgatt 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 aagtgtatgcacgtgtgcctgtgttgtgccaacattgatatcatgacgagcatgatg 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STSYGTECYVPOSA"
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7.0%; Score 62.2; DB 16; Length 34094;
Best Local Similarity 45.0%; Pred. No. 3.2e-07;
Matches 317; Conservative 0; Mismatches 383; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(33398. .33401)
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TATA_signal
repeat_region
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INCTLDRGPEREY SCTARALLALER Y VURLEY BY THE GLANGGDRRYLDMASTFFD
INCTLDRGPEREY SCTARALLALER SAPNING YLDRGET EAGKVINT RAGASTRGEND
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27976. .28602
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Campbell, J.B. and Zhao, Y.
Complete DNA sequence and genomic organization of canine adenovirus
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Direct Submission
Direct Submission
Submitted (02-NOV-1996) Campbell J.B., University of Toronto,
Mcdocal Genetics and Microbiology, 150 College Street, Toronto,
Mcdocal Genetics and Microbiology, 150 College Street, Toronto,
Ontario M5S 3E2, Canada
Nomenclature of proteins has largely followed accepted terminology
Nomenclature of proteins has largely followed accepted terminology
of the human adenovituess.

Location/Qualifiers
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                                                                                   31872 GGGCGCGAC -- GCTGTGGAACTTTCATTGCCACTGTCTGAAAAGGTCCAGTCTGGAGTGC 31815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    763 gaggagecactgccatgttgtattcctgcaggacggaggcggcggcagcagtttatt 822
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                                       343 catggttacgagtcctgggctctccactgtcattgttccagtcccggttccctgcagtgt 402
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1. 198
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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GAPPNTERLEIYYDVETYTWHGREGGOLPFMLYPOLLGDHHYNVARTLAFEQNWEI
LESPEELTPOOLKEKEKKERNERDFENLOOHTAASIWSHYICQOEKATTLG
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KOGKVFLIKDISQMQKCEFCGSFFKVTHTCALRRNDFYFHHVAAHSADWWEKISFTPI
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/function="structural protein"
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/function="virion assembly"
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SGS

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/translation="MQBEECVPTCTKAWGSLCLARCPVKPSSDKLFLFISKAMAILIS
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Canine adenovirus type 1.

Viruses; dSDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

1 (Dass 1 to 199)

Sira, S., Abouhaidar, M.G., Liu, Y.C. and Campbell, J.B.

Multiple reiteration of a 40-bp nucleotide sequence in the inverted virology 159 (1), 76-83 (1987)
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Canine adenovirus type 1 E1A protein, small T-antigen, large
T-antigen, protein IX, IVa2 protein, DNA polymerase, pTP, 52-55K
protein, Pilla, penton base protein, pVII protein, pV protein, M
PEA-DBP, 100 KD protein, L4-22KD protein II, endoproteinase, virion component IV, U-exon, E4 orf5, E4 orf4, E4 orfein, pVIII, and E.A. orfil genes, complete cds.
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Campbell,J.B. and Zhao,Y.
DNA sequence and genomic organization of canine adenovirus type 1
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11.1%; Pred. No. 0.0013;
Ive 0; Mismatches 112; Indels 0;
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17; Conservative
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Best Local Simil
Matches 117; C
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KINE ME KRUCKLIE NUL II SULPUPES V VENUIR KHWEGGEV LASDUKTUUZ I KEWWINDIE SU
THTSEKNAARAS EZIVSKGCEP YORONDETMIGSYOODAGEPDIKYWKODEETZENK
THTSEKNAARAS EZIVSKGCEP YORONDETMIGSYOODAGEPDIKYWKODEETZENK
DLWRKEKKOAYD I GOGTUSCALDYOYTAOLYNKILESYOI FIRNSVULPETY FNVFO
RPILSS NSHAIFOOLIY RAEKPNAPHLINT I IMAPSKBRYETSYLES IRKGKCEYTY I GY
LOEDYLY YOD THE TOOTA SALTHPF PAGSPLNYY ERAYAIKAY HAY DHENTY TSTPEDELL
PGIPTIDADPPABEELJOLPPECSRKGGRLCWT NEPLRGEYTTSIDVITLHNRGWY Y
LI PDIRTTY VEPRWACCLAREYOLNIA MEKEKNEKNSK KONTRSITALSONALVESFATKL
DNKRTVF SOOIESNIA KEIASGAYVVK SSY I ETDNLCAETHEEVYAY PPVNFDVHR
LAPPSY SEETPTEN HAAGEPRONIN MEKEKNEKNIKKSY VOOPUSELTTMEGY
NNRYASOI LASTYAMTRAFYSEWSOPLY ENDAGIP LEKSTIKKSY VOOPUSELTTMEGY
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TSYOTHVOPETYTETTLIRKLRPWKDKTLHALDMNRLIPYSRKY PNPRNNETTWMELO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MHPVLKOMKPLPASVVKLEAESEGLARLOGGAAPEVHPRVQMKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSRIKYTEIHLPLOOKLINTYMANGSYTINTGAYHREIDFERFEETLAQVOOAVLAE
RVVADLALIRPMRGYGTTNMAGDRQVPVEGLLODHYKNLSGCONHAMGLADBMRIONA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="aab05435.1"
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                                                                                                                                                                                                                                                                                                                                                                             KQPFIAAVYGPTGCGKSQLLRNLMSAQLIVPTPETVFFITPQVDMIPPQEIAAWETQI
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by comparison with human Ad2"
/note="splice site tentative, by comparison with human Ad2"
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                                                                                                                                         Campbell, J.B.
Direct Submission
Submitted (14-APR-1996) James B. Campbell, University of Toronto,
Submitted (14-APR-1996) James B. Campbell, University of Toronto,
Microbiology, 150 College Street, Toronto, Ontario, Canada, M55 1A8
Nomenclature of proteins has largely followed accepted terminology
of the human adenoviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence-experimental
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/note-similar to human Ad Ela 298R protein; splice site
by comparison with canine adenovirus type 2: Shibata et
al., Virology 172 (1989) 460-467."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="40-base pair repeat not found in other strains canine adenovirus type 1; field isolate: Spibey et alvirus Research 14 (1989) 241-256."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(3502. .4829,5108. .5120)) /function="virion assembly"
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1. .30288
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/function="inhibition of apoptosis"
/note="ElB 19kD protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3174. .3485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1768. .3102
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| . 159
/note="left ITR"
54. 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /citation=[3
                                                                    Unpublished
4 (bases 1 to 30288)
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हरप्रहर -----

10 mm

CDS

CDS

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rnerieravsgarorelndrelmyrlrealtsnglseieggedsarvrskenwgagag
Vgaasaryphlldyeekenpdgsvsfqqhergtqshengghaepaysrrolgrfy"
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CDS

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Gaps Query Match
5.5%; Score 48.4; DB 16; Length 30288;
Best Local Similarity 50.4%; Pred. No. 0.0032;
Matches 118; Conservative 0; Mismatches 116; Indels 0;

ö

DD 28076 TGGCAAGTACATTGTCACTGTTCTTTGCAATGTCTGCTACGCAA 28017 .. 358 tgggctctccactgtcattgttccagtcccggttccctgcagtgtatagccggcggcag 417 ð

28016 Gritiaaaagaaiticiigaagaatiigiaaiggiggiggiggiggiggagaaaaagaicii 27957

TDb 27956 IGGTACCGAGAGTTTGTGAATTCTAGCAGCCTGATGAGATTAATGTGGGGGGGAGTATA 27897 ...478 tggtaccgggaggtggtgaattacaacatgccaaagagtaatgtttatgtccagcgtg 537 g 8

DD 27896 AIGITIAGAARCAITCATIACATITAGACTGTCTTTTTTTAGCACCGTG 27843

Search completed: June 23, 2000, 09:34:53 Job time: 12475 sec

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OM nucleic

Run on:

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Purectors:

Disclosure; Page 37-39; 69pp; French.

Disclosure; Page 37-39; 69pp; French.

This is the sequence corresponding to nucleotides 32749-35935 of the funan adenovirus type 5 (Ad5), which covers the E4 and right inverted than adenovirus type 5 (Ad5), which covers the E4 region of the companies. The E4 region of the edenovirus late genes. The E4 region of the edenovirus late genes. The E4 region is covered to generate cell lines, esp. 293 cells, which can support the compliant of defective recombinant adenoviruses, esp. those that Lack.

Covered to generate cell lines, esp. 293 cells, which can support the condition of defective recombinant adenoviruses, esp. those that Lack.

Covered inserted into their genomes for complementation of the defective region inserted into their genomes for complementation of the defective viruses are esp. mentioned in the specification: they allowed the E4 region and part of the E4 region; virus AVI completelies (nts) 34801-3439 and 34415-33126 consisting of completelies (nts) 34801-3439 and 34415-33126 consisting of completelies (nts) 34801-3439 and 34415-33126 consisting of completelies (nts) 34801-34355 and 444 further lacks the C6 research as nts 33093-33695 and 3463-33555 and AV4 further lacks the completion viruses generated in the new cells can be used for gene completion disorders, virus dystrophy, encodegenerative diseases, chlose defective viruses yer. Growers, dystrophy, encodegenerative diseases, chlose defective viruses yer. Growers (new colls can be used for gene complete also be.
          Human secreted pro
HSV-2 strain SB5 C
O. sativa Xa21
HSV-2 strain SB5 C
Sequence encoding
Cellular transcrip
Measles virus AIK
ceff (ORF9) encodi
Green fluorescent
Cephamycin biosynt
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Adenovirus E4 and part ITR region corresp. to bases 32749-35935.
Human adenovirus; inverted tandem repeat; E4; E1; open reading frame; expression; late gene; cell line; defective recombinant adenovirus; complementation; gene therapy; cystic fibrosis; dystrophy; ds; neurodegenerative disease; blood coagulation disorder; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 96-354535/35.
Cells for prodn of recombinant adeno and adeno-associated virus
contain part of the E4 region of adeno virus, used to produce new
adeno virus defective in E1 and E4 regions for use as gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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C, Perricaudet M, Vigne E;
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100.0%; Pred. No. 6.8e-269;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
V18266
V34209
V62169
X23525
V62176
Q9456
Q10093
V18271
T00591
V71079
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20-JAN-1995; FR-000747.
01-JUN-1995; FR-006532.
08-SEP-1995; FR-010541.
(RHON ) RHONE POULENC RORER SI
Dedieu J, Latta M, Orsini C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 885; Conservative
  15894
3301
6385
9424
117213
7326
7326
15894
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WPI; 96-354535/35.
     Adenovirus Ad5.
WO9622378-Al.
25-JUL-1996.
     332.2
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Explete DNA seque
Bovine adenovirus
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Measles virus Edmo
Measles virus Rube
Measles virus Mora
Measles virus Zagr
Measles virus 1977
                                                                                                                                                                                 June 23, 2000, 09:05:32 ; Search time 56.99 Seconds (without alignments) 3885.243 Million cell updates/sec
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Chimpanzee adenovi
Adenovirus 17. Rec
Chimpanzee adenovi
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Second generation
Chimeric plasmid p.
Complete sequence
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Adenovirus 5 genom
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Human Id-1H gene.
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                                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Database :

Result

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1521. .2405 /*tag= b /product= human A

terminator sequence"

gene

/*tag= c /note= "growth hormone

Gao G, Wilson JM;

010245.

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Ferench mant adeno-associated virus contg. second gene which

Facilitates its conversion from single stranded to double stranded

Facilitates its conversion from single stranded to double stranded

Formus - enhances efficiency of ex vivo transduction into target cell

Family - its is the nucleotide sequence of a minigene containing the human

Control of the mouse mammary tumour virus promoter and a growth hormone

Control of the mouse mammary tumour virus promoter and a growth hormone

Control of the mouse mammary tumour virus promoter and a growth hormone

Control of the mouse mammary tumour virus promoter and a growth hormone

Control of the mouse mammary tumour virus promoter and a growth hormone

Control of the mouse mammary tumour virus promoter and a growth hormone

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(UYPE-) UNIV PENNSILVANIA.
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vivo;

13-7405. 27-AUG-1997 (first entry)
Plasmid pMMTVE4ORF6 minigene sequence.
Minigene; human adenovirus type 5; open reading frame; promoter; in v mouse mammary tumour virus; growth hormone; terminator; recombinant; packaging cell line; adeno-associated virus; ex vivo; gene therapy; inherited disease; cancer; genetic dysfunction; cystic fibrosis; ds.

T59270 standard; cDNA; 3653 BP. T59270;

Location/Qualifiers
1. .1506
/*tag= a
/note= "mouse mammary tumour virus promoter"

Synthetic. promoter

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12-DEC-1996.
04-JUN-1996; U10245.
05-JUN-1995; US-462014.
27-CT-1995; US-549489.
(UYPE-) UNIV PENNSTLVANIA.
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Second generation recombinant adenoviral vector pAV.CMVALP.GRE-ORF6.
Second generation recombinant adenovirus type 5; open reading frame; promoter; in vivo; Minigene; human adenovirus type 5; open reading frame; promoter: no vivo; mouse mammary tumour virus; growth hormone; terminator; recombinant; packeging cell line; adeno-associated virus; ex vivo; gene therapy; inherited disease; cancer; genetic dysfunction; cystic fibrosis; ds.
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note- "glucocorticoid dependent promoter GRE"
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4315. .4713
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/rpt_type= inverted
/note= "5' AAV ITR"
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/note= "3' AAV ITR"
4714. .8299
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Figher KX, Gao G, Wilson JM;

WET; 97-043152/04.

WET; 97-043152/04.

PT Recombinant adeno-associated virus contg. second gene which recombinant adeno-associated virus stranded to double stranded to facilitates its conversion from single stranded to double stranded to transfer set filters of ex vivo transduction into target cell virus - enhances efficiency of ex vivo transduction into target cell to virus set 108-114; 131pp; English.

Example 19; Page 108-114; 131pp; English.

CC adeno-associated virus (rAAV) which contains 2 genes, the first gene can be to express the gene of interest (beta-qabactosidase) in the target cell; and the second gene of interest (beta-qabactosidase) in the target cell; and the second gene of interest (beta-qabactosidase) in the target cell; and the stended virus to its double stranded form upon expression. The rAAV is stranded virus to its double stranded form upon expression. The rAAV is useful in pharmaceutical compositions for use in ex vivo and in vivo gene converting to the treatment of inherited diseases, cancer and other genetic converting adeno-associated interest and page of a recombinant adeno-associated interest converting the converting converting the converting
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VC 74214;
VC 7421
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F. 04-SEP-1997; U15694.

R. 06-SEP-1997; U15694.

R. (UYPE-) UNLY PERNSTLVANIA.

Tarina SF, Fisher KJ, Wilson JM;

R. WFI: 98-195635_AT.

Chimpanzee adenovirus vector - useful in gene therapy and genetic rengineering in general

S. Example 4, Pages 89-94; 116pp; English.

C. The sequence is that of plasmid pAV.CMVALP.GRE-ORF6, also called avoirfs, which generates a recombinant adeno-associated virus containing the Lacz transgene and the adenovirus E4 ORF 6.

Sequence 8299 BP; 1816 A; 2130 C; 2108 G; 1963 T;
aggacaaggcgccttatgctgcgggcggtgcgaatcatcgctgaggagaccactgccatg
                                                                                                            /*tage c // fote- "human placenta alkaline J 2893. .3990 /*tag- d // fote- "SY40 polyA signal"
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/note= "AAV inverted terminal
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/*tag- 9
/note- "SV40 polyA signal"
4547. .4713
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                                                             cggcgcactccgtacagtagggatcgtctacctccttttgagacagaaacccgcgctacc
                                                                    7/37370 standard; DNA; 8710 BP.
V32370;
29-SEP-1998 (first entry)
Complete sequence of the pE4/Hygro plasmid.
Circular; adenovirus type 5; pE4/Hygro plasmid; structural protein; complementation; E4 regulatory protein; gene therapy; HIV; tumour;
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      Length 8299;
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100.0%; Pred. No. 1.1e-268;
iive 0; Mismatches 0;
Query Match 100.
Best Local Similarity 100.
Matches 885; Conservative
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V32370/c
ID V323
AC V323
DT 29-SI
DE COMP
KW Circi
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V. 6. V. A. .

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1757 GCTCTCCACTGTCATTGTTCCAGTCCCGGTTCCCTGCAGTGTATAGCCGGGCAGGTT
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          KW Huntington's disease; Tay-Sachs disease; sickle cell disease;

KW marly gene; ds.

Synthetic.

ET misc_feature complement (707. 3820)

FT misc_feature (3830. 6470

FT misc_feature (3830. 
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tive 0; Mismatches 0;
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Matches 885; Conservative
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WPI; 98-230709/20.
Adenoviral vectors - which lack DNA encoding for structural protein 'or fibre protein used particularly for gene therapy

Example 1; Pages 131-145; 170pp; English.
The present sequence is that of a pE4/Fiber plasmid used in the method of the invention. The plasmid contains an adenovirus type 5 (AD5) method of the invention. The plasmid contains an adenovirus fiber gene controlled by a CMV promiter, an AD5 E4 gene and an adenovirus type 2 (AD2) tripartite leader sequence upstream of the fiber gene. The invention provides adenoviral vectors having deletions of all or part of
                                                                                                                                                     Complete sequence of the pE4/Fiber plasmid. structural protein; circular; adenovirus type 5; pE4/Fiber plasmid; structural protein; complementation; fiber protein; gene therapy; HTV; tumour; AD5; early gene; Huntington's disease; Tay-Sachs disease; sickie cell disease; E4 regulatory gene; ds.
                                                                                                                                                                                                                                                                                                        ttgtattcctgcaggacggaggggggggggggggtttattcgcgcgctgctgcagcac
                                                                         /*tbg= a /note= "ADS E4 regulatory gene" 4051. 4366 /*tag= b /note= "ADS leader sequence" 4372. 6124
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/note= "AD5 fiber gene"
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complement (21. .3149)
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V32375;
29-SEP-1998 (first entry)
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24-SEP-1995; E05251.
25-SEP-1996; US-719806.
(NOVS ) NOVARTIS AG.
(SCRI ) SCRIPPS RES INST.
MEMBEROW GR, VON SEGGERN DJ;
WPI; 98-230709/20.
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carly region proteins. Deletions in these proteins would allow a reduced risk of wild-type virus contamination and would allow a packaging of foreign DNA in such vectors for a variety of diagnostic and therapeutic applications. The adenoviral vectors having deletions in the structural and/or early gene regions are produced by cellular complementation of these adenoviral genes. Therefore, the pE4/Fiber plasmid was used as a complementation plasmid which was introduced into plasmid was used as a complementation plasmid which was introduced into a host cell line where parts of the fiber and E4 gene region would be stably inserted into the host cell chromosomes. The resulting E4/fiber vectors can be used for diagnosis or gene therapy, e g. for treating conditions characterised by hyper-proliferative cells (e.g. tumours), sockie cell diseases (e.g. Huntington's disease, Tay-Sachs disease, or sickie cell disease), or infections (e.g. Huy Infection). They can also be used for in vitro production of biologically active proteins.
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  gene sequences encoding adenoviral
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666 TIGIATICCIGCAGACGAACGGCGCGCGCACAGTITATICGCGCGCIGCIGCAGCAC 607 726 AGGACAAGGCGCCTTATGCTGCGGGCGGTGCGAATCATCGCTGAGGAGCCACTGCCATG 781 ttgtattcctgcaggacggagcggcggcagcagtttattcgcgcgctgctgcagcac 160559;
05-MAR-1998 (first entry)
Recombinant adenovirus H5.020TKneo-int.
Adenovirus H5.020TKneo-int, plasmid pAdMLVneo-int; Ad5; Mo-MLV;
retrovirus; retrotransposition; transposition; transposition; cetrovirus; vector; neomycin resistance; neo gene; ss.
Chimeric - Mastadenovirus serotype 5.
W09715679-A1. 6624 8873 G; 841 caccgccctatcctgatgcacgattatgactctaccccatgtag 9141 C; T60559/c ID T60559 standard; DNA; 32026 BP. 7388 A; MOYALLOON MAY 1997.
24-OCT-1996; U17176,
27-OCT-1995; U5-005942.
(UYPE-) UNIV PENNSTLYANIA. à 셤 à 셤

Query Match
100.0%; Score 885; DB 1; Length 32026;
Best Local Similarity 100.0%; Pred. No. 2e-268;
Matches 885; Conservative 0; Mismatches 0; Indels 0; Gaps

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                                                                                  Location/Qualiflers
8772. 9385
/*tag= a
/note= region deleted in plasmid pdepTP
pBHGildelpTP (Claim 45)"
8773. 9586
                                                                                                                                                                                                         V07261 standard; DNA; 34303 BP.
V07261;
28-SEP-1998 (first entry)
Adenoviral vector plasmid pBHG11.
Adenovirus 5; Ad5; vector; gene therapy;
Mastadenovirus 5.
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V07261/C
AC V07261 standar:
AC V07261
DT 28-SEP-1998 (:
DT 28-SEP-1998 (:
DT Adenoviral very
KW Adenoviral s;
OS Mastadenovirus S;
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30-APR-1997; U19541.

30-APR-1999; U19541.

23-OCT-1995; U5-735609.

23-OCT-1996; U5-735609.

23-OCT-1996; U5-735609.

23-OCT-1996; U5-735609.

24 malfitten A, Chamberlain JS, Hartigan-Oconnor DJ, Hauser MA, Kumar-Singhr:

15 malfitten A, Chamberlain JS, Hartigan-Oconnor DJ, Hauser MA, Kumar-Singhr:

16 malfitten A, Chamberlain JS, Hartigan-Oconnor DJ, Hauser MA, Kumar-Singhr:

17 malfitten A, Chamberlain JS, Hartigan-Oconnor DJ, Hauser MA, Kumar-Singhr:

18 WI; 98-261485/23.

18 WI; 98-261486/23.

18 MI; 98-261486/23.

20 MI; 98-261486/23.

21 MI; 98-261486/23.

22 MI; 98-261486/23.

23 MI; 98-261486/23.

24 MI; 98-261486/23.

25 MI; 98-261486/23.

26 MI; 98-261486/23.

27 MI; 98-261486/23.

28 MI; 98-261486/23.

29 MI; 98-261486/23.

20 MI; 98-261486/23.

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32446 ArgacracGrccGGGGTTCCATTTGGCATGACACACCACCAACACGATCTCGGTTGTCT 32387
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/*tag= b
/note= "region deleted in plasmid
/note= paxBdelpoidelpTPVARNA+ti3 and
pBHGildelpoiydelpTPVARNA+ti3 (Claim 53)'
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Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 885; Conservative 0; Mismatches 0;
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Sequence 34303 BP; 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant adenovirus Ad:Pac-beta-Gal.
Recombinant adenovirus Ad:Pac-beta-Gal.
Recombinant adenovirus Ad:Pac-beta-Gal, replication deficient adenovirus,
Bla region, E3 region, gene therapy, nitric oxide synthetase; NoS;
cystic fibrosis chloride channel; LDL receptor; erythropoietin;
atherosclerotic artery; ss.
Mastadenovirus.
                                                                                                                         32206 TGGGALATGGTTCTAACGCGGGAGGAGCTTGTAATCCTGAGGAAGTGTATGCACGTGTGC 32147
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"R 17-JAN-1995; US-374483.
"A (UTDU-) UNIV DUKE.
"B ALGOIGE SE;
"R PPSDB; W97243.
"T WPT; 99-204005/17.
"R P-PSDB; W97243.
"T New replication deficient adenovirus bearing deletions of the Ela FI and E3 regions - containing a single packaging signal sequence and PT and E3 regions - containing a single packaging signal sequence and PT and is useful as a gene therapy vector.

PT and is useful as a gene therapy vector.

PS Disclosure; Fig 49-100; 148pp; English.

CC The present sequence represents recombinant adenovirus

CC Ad:Pac-Deta-Gal, which exemplifies the invention. The specification
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                                                                                                                                                                                                                                                             32026 TIGGCCAGCTGGTTAGGATGGTGGTGGTGGCCCCATGTTTAATCAGAGGTTTATATGG
                                                                                                                                                                   301 ctgfgttgtgccaacattgatatcatgacgagcatgatgatccatggttacgagtcctgg
                                                                                                                                                                                                                                                                                                                                                                                                  ttggccagctggtttaggatggtggtggatggcgccatgtttaatcagaggtttatatgg
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X15627 standard; DNA; 34382
X15627;
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AC XIII
AC XI
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the Ela and E3 regions and comprises asingle packaging signal sequence and Eas and E3 regions and comprise a single packaging signal sequence and the Ela deletion contains at least one Paci, Clai, Xbal Card East one Paci, Clai, Xbal Card East of East one Paci, Clai, Xbal Card StBi cleavage site. The replication deficient viral vectors can be molecules of therapeutic importance, including isoforms of the nitric cystic fibrosis chloride channel (CFTR) gene, the dystrophin gene, the LD receptor gene and the erythropoietin gene. The NOS isoforms can be used in vascular applications or in cancer therapy (microphage NOS), The Cornary artery bypass grafts. A NOS containing adenovirus can also be the concary artery bypass grafts. A NOS containing adenovirus can also be catherosclerotic arteries.

Sequence 34382 BP; 7923 A; 9880 C; 9421 G; 7158 T;
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replication deficient adenoviruses having deletions of
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Pred. No. 2.1e-268;
0; Mismatches 0;
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100.0%;
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Best Local Similarity 100.
Matches 885; Conservative
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Conservative

Matches 885;

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781 ttgtattcctgcaggacggacggcggcagcagcattattcgcgcgctgctgcagcac 840
                31438 CACCGCCCTATCCTGATGCACGATTATGACTCTACCCCCATGTAG 31394
             841 caccgccctatcctgatgcacgattatgactctacccccatgtag
                            RESULT 10
X07371/c
ID X07371 standard; DNA; 34427
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100.0%; Score 885; DB 1; Length 34427; 100.0%; Pred. No. 2.1e-268;

Query Match Best Local Similarity

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DD 32569 AIGACIACGICCGGCGIICCAIIIGGCAIGACACIACGACCAACACAACACGGIIGICI 34510'
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                                                                          32509 cGGCGCACTCCGTACAGTAGGATCGTCTACCTCCTTTGAGACGGAAACCCGCGCTACC 32450
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                                                 cggcgcactccgtacagtaggatcgtctacctctttgagacagaaacccgcgctacc 120
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1 atgactacgtccgcgttccatttggcatgacatacgaccaacacgatctcggttgtct 60
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Recombinant cis-acting adenovirus H5.020TKneo-int(LTR).
Adenovirus H5.020TKneo(LTR); plasmid pAdMLVneo-int;
Adenovirus; retrotransposition; transposition; transgene;
gene therapy; vector; neomycin resistance; neo gene; ss.
Chimeric - Mastadenovirus serotype 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               841 caccgocotatoctgatgcacgattatgactctaccccatgtag 885
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T60557/C
T60557/C
T60557 standard; DNA; 35000 BP
AC T60557; Standard; DNA; 36000 BP
AC T60557; Standard; DNA; 36000 BP
DE Recombinant cis-acting adenovi
KW Adenovirus H5.020TKneo(LTR); p
KW retrovirus; retrortransposition
KW gene therapy; vector; neomyotin
OS Chimeric - Mastadenovirus sero
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WARL 39-7-28901/23.

PT MOST cell chromatin in the presence of transposase, providing stable by the durable transgene expression

PS ARMPNE 2; Fig 8A-1; 74pp; English.

This is the DNA sequence of the cis-acting recombinant adenovirus

CC This is the DNA sequence of the cis-acting recombinant adenovirus

CC This is the DNA sequence of the cis-acting recombinant adenovirus

CC This is the DNA sequence of the cis-acting denovirus (see 150558) was also produced, and trans-acting adenovirus (see 160558) was also produced, and retrotransposition and integration viruses. Claimed novel recombinant replication defective viruses of the bost cells was demonstrated in HeLa cells infected with both of viruses. Claimed novel recombinant replication defective viruses (A) comprise: (a) DNA of, or corresponding to, at least part of the virus acquence (ES) comprising a human gene (I) linked to virus geneme, able to infect a mammallan cell; and (b) a first expression sequence (ES) comprising a human gene (I) linked to the cis-acting terminal repeat sequences of a transposon, and ESI express (I) and transfer it to the cellular chromatin in vivo or in recombinant replication defective virus (B) containing a trans-acting express (I) and transfer it to the cellular chromatin in vivo or in recombinant replication defective virus (B) containing a rans-acting recombinant replication defective virus (B) containing a rans-acting and a second expression sequence (ES) containing a trans-acting containing a cells; and containing a mammalian cells which stably express (I) integrated into its conformed with contact of the conformation in the presence of claimed).

CC delivery and stable integration of (I) into a host cell defects or recombinant retroviruses (RW) (claimed).

CC claimed).

CC claimed over an expected defects or recombinan
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  - Moloney murine leukaemia virus.
- Rattus sp.
- Synthetic.
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                                                                                                      U1-MAY-1997.
24-OCT-1996; U17176.
27-OCT-1995; US-005942.
(UTPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                              Kelley WM, Wilson JM;
WPI; 97-259031/23.
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ö 0; Gaps 1. atgactacgtccggcgttccatttggcatgacactacgaccaacagattcggttgtct uery_Match.
100.0%; Score 885; DB 1; Length 35000; est.local..Similarity 100.0%; Pred. No. 2.1e-268; Efchesr...885; Conservative 0; Mismatches 0; Indels 0;

DE 33142 AIGACTACGICCGGCGTICCATIIGGCAIGACACIACGACCAACACGAICTCGGIIGIIII ð g

tacgtgcgaggtcttccctgcagtgtgggatttacgctgattcaggaatgggttgttccc 181 셤 à 셤

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32782 GCTCTCCACTGTCATTGTTCCAGTCCCGGTTCCCTGCAGTGTATAGCCGGCGGCGGCAGGTT 32723 361 gctctccactgtcattgttccagtcccggttccctgcagtgtatagccggcggggaggtt 42b taccgggaggtggtgaattacaacatgccaaaagaggtaatgtttatgtccagcgtgttt ttgtattcctgcaggacggagcggcggcggcagtttattcgcgcgctgctgcagcac 721 aggacaaggogccttatgctgcgggoggtgcgaatcatcgctgaggagaccactgccatg 481 781 ద ద ŏ g ò g ö g ò a δ 셤 셤 ò à

23-0cr-1997; U19541.
23-0cr-1996; US-735609.
(UNMI) UNIV MICHIGAN.
Halfitano A, Chamberlain JS, Hartigan-OConnor |
Hauser MA, Kumar-Singhr;
WPI; 98-261485/23. Adenovirus 5 genome. Adenovirus 5; Ad5; vector; gene therapy; ds RESULT 12 V07258/c Th V07258 standard; DNA; 35935 V07258; 28-SEP-1998 (first entry) Mastadenovirus 5. 30-APR-1998.

While Scientific Procession of large foreign DNA fragments, used for, e.g. gene therapy of generic classes(s)

Therapy of generic classes(s)

Disclosure; Page 69-86; 139pp; English

The invention provides improved adenoviral vectors and packaging reliable.

This nucleotide sequence comprises the adenoviral sectors and packaging reliable invention provides improved adenoviral vectors and packaging within the E2b region of the adenoviral genome (see also VO7261).

These E2b-deleted virus are used in conjunction with novel cell ines that constitutively express E2b gene products. The invention species deleted for all viral coding regions. These is sho provides vectors deleted for all viral coding regions. These is both occlis, as demonstrated by the transfer of the dystrophin gene to the muscle of mice. The E2b-deleted and gutted vectors can be provide improved adenoviral vectors useful for a wide variety of gene therapy applications.

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24-CCT-1996; U17176.
27-CCT-1995; US-005942.
(UYPE-) UNIV PENNSTLVANIA.
KELLEY WM. WILSON JM;
WPI; 97-259031/23.
                                                                                                                                                                                                                                                             retrovirus.
36538 BP;
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Best Local Similarity
Matches 885; Conserv
                                     01-MAY-1997
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Sequence
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                                                      cggcgcactccgtacagtagggatcgtctacctcctttgagacagaaacccgcgctacc 120
                       Gaps
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           Length 35935;
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T60558, standard; DNA; 36538 BP.
AC T60558,
DT 05-MAR-1998 (first entry)
DE:..'Recombinant trans-acting adenovirus H5.020CMVgag-pol.
           Query Match 100.0%; Score 885; DB 1; L
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 885; Conservative 0; Mismatches 0;
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nost cell orrowatin in the presence of transposory processing and durable transgene expression

Example 2; Fig 9A-1; 74pp; English.

Example 2; Fig 9A-1; 74pp; English.

Example 2; Fig 9A-1; 74pp; English.

However, a sequence of the trans-acting recombinant adenovirus (see Fig. 020cMvgag-pol. It was obtained by co-transfecting HEK293 (arc CRL1573) cells with linearised plasmid padGMvgag-pol (see Fig. 020cMvgag-pol.) at was obtained by co-transfecting HEK293 and AdSI7001.

Calso produced, and retrotransposition and integration into host cells was demonstrated in HeLa cells infected with both viruses.

Calso produced, and recrotransposition and integration into host cells was demonstrated in HeLa cells infected with both viruses.

Calso produced, and recrosponding to, at least part of the cells was demonstrated in HeLa cells infected with both viruses.

Capression sequences for expression, with the cassette flanked by required for expression sequences for expression, and ESI comprising a human gene (1) linked to required by DNA of (a); (A) can infect a mammalian cell and can capilatory sequences for expression, with the cassette flanked by Capression defective virus (B) containing a transposase (I) and transfer it to the cellular chromatin in vivo or in capped as perplication defective virus (B) containing a trans-acting and a second expression sequence (ES) containing a trans-acting cromatin, produced by infection with (A). (A) and (B) are used contomatin, produced by infection with (A). (A) and (B) are used contomatin, produced by infection with (A). (A) and (B) are used contomating a cellivery and stable integration of (I) into a host cell command a such as cystic fibrosis. (A) and (B) are used contomating terroviruses (RNV) (claimed). (A) and (B) are used contomation at erroviruses (RNV) (claimed). (A) and (B) are used contomation as action as a very produced administration is avoided organ the read of or repeated administration is avoided. The transgene is inherited by the progeny cells and the viral compon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant replication defective virus - inserts transgene into host cell chromatin in the presence of transposase, providing stable
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Adenovirus H5.020CMVgag-pol; plasmid pAdMLVneo-int; Ad5; Mo-MLV; retrovirus; retrotransposition; transposition; transgene; gene therapy; vector; ss. Chimeric - Mastadenovirus serotype 5. Chimeric - Moloney murine leukaemia virus. Chimeric - Cytomegalovirus.
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11arity 100.0%; Pred. No. 2.2e-268;
Conservative 0; Mismatches 0;
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34440 TGGGATATGGTTCTAACGCGGGAGGAGCTTGTAATCCTGAGGAAGTGTATGCACGTGTGC 34381
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Glucocorticoid receptor/adenoviral ORF6 chimaeric fusion gene.
Glucocorticoid receptor/adenoviral ORF6 chimaeric fusion gene.
Human adenovirus; inverted tandem repeat; E4; E1; open reading frame; expression; late gene; cell line; defective recombinant adenovirus; complementation; gene therapy; cystic fibrosis; dystrophy; ds; pcR; neurodegenerative disease; blood coagulation disorder; viral infection; primer; amplification; polymerase chain reaction; fusion protein.
Homo sapiens/Adenovirus Ad5.
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                                                                                                             ttggccagctggtttaggatggtggtggatggcgccatgtttaatcagaggtttatatgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucocorticoid receptor/adenovirus Ad5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           841 caccgccctatcctgatgcacgattatgactctacccccatgtag
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product fusion protein
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1. 1605
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19-JAN-1996; F00088.
20-JAN-1995; FR-000747.
01-JUN-1995; FR-006532.
08-SEP-1995; FR-010641.
(RHON ) RHOME POULENC RO Dedieu J, Latta M, Ors WPI: 96-354335/35.
P-PSDB: W03197.
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Db. 34160 A

Db. 34080 G

Oy 661 G

Oy 661 G
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The invention relates to novel cell lines which can support the farauges of the invention relates to novel cell lines which can support the replication and production of defective recombinant adenoviruses which lack all or part of the El and Ed regions. The novel cell lines contain the adenoviral Ed region, esp. the open reading frame 6 and/or 7, or inserted into its gene under control of a promoter, pref. from MMTV which is required by dexamethasone. The Ed ORFG may also be inserted into the genome as a chimaeric fusion gene (this sequence) comprising a quency of the cell in the absence of hormone by interaction of the cytoplasm of the cell in the absence of hormone by interaction of the cytoplasm of the fusion protein with the hormone causes translocation of the protein to the cell's nucleus were the ORFG product functions. The contacting the fusion protein with the hormone encoding the hormone binding domain with the hormone encoding the hormone. Contacting the fusion protein with the hormone encoding the hormone causes translocation of the adenoviral order sequence. The defective viruses generated in the convention of the adenoviral order sequence. The defective viruses generated in the convention of the adenoviral order sequence. The defective viruses generated in the conventions, etc.

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virus defective in El and E4 regions for use as gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tacgtgcgaggtcttccctgcagtgtgggatttacgctgattcaggaatgggttgttccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 883.4; DB 1;
Pred. No. 1.7e-268;
0; Mismatches 1;
                                                       Example 1; Page 40-41; 69pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.9%;
Matches 884; Conservative (
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WUMPALLOADY-A.

PD 09-JUN-1994.

U1667.

PR 03-DEC-1992; U1667.

PR 01-OCT-1992; US-985478.

PR 01-OCT-1993; US-136682.

PR 13-OCT-1993; US-136742.

PR 14-ORD COULUME LA, Gregory RJ, Smith AE;

WPI; 94-200277/24.

PR Adeno:virus-based gene therapy vectors - esp. useful for gene

PR Adeno:virus-based gene therapy vectors - esp. useful for gene

PR Adeno:virus-based gene therapy vectors - esp. useful for gene

PR Adeno:virus vector for the second generation

C Lang sequence represents the nucleotide sequence of the second generation

C This sequence represents the nucleotide sequence of the second generation

C Adenovirus vector named Ad2-ORF6/PGK-CFTR. This virus lacks E and in its

C Dace conteains a modified transcription unit with the phosphoglycerate

C C Adenovirus vector and a poly A addition site flanking the cystic

C Librosis transmembrane condutance regulator (GFTR) CDNA. The POK

C fibrosis transmembrane condutance regulator (GFTR) CDNA. The POK

C fibrosis transmembrane condutance regulator (GFTR) cbnA. The POK

C fibrosis transmembrane sequence has also been modified

C subject to shut off. The E4 region of the vactor has also been modified

C un that the whole sequence has been removed and replace by ORF6, the

C only E4 gene essential for growth of adenovirus (Ad) in tissue culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= 2
/note= Represents residues 1-12914 of pAd2/PGK-CFTR"
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Jnote- "major late mRNA L4 poly-A signal (putative)"
31051. 31530
/*tag- u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note "major late mRNA L5 poly-A signal (putative)"
                                                                                                                                                                                      /note= "Major late mRNA L3 poly-A signal (putative)" complement (244729. .26318)
"major late mRNA L2 poly-A signal (putative)". 20992
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/note= "E3-2 mRNA poly-A signal (putative)"
35013. .35018
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/note- "Glycosylated membrane protein"
31707. .32012
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Hexon-associated precursor" 30444. .30449
                                         /*tag= n
/product= pVI protein
/note= "Hexon associated precursor"
21077. .23983
                                                                                                                                                                                                                                                     "tag" q
/product = DBP protein
/note= "DNA binding or 72K protein"
26347. .28764
                                                                                                                 /*tag= 0
/product= Hexon protein
/note= "Virion component II"
24657. .24662
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/product= 100K protein
/note= "Hexon assembled"
29454. .30137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= aa
/note= "pgk promoter"
1011. 5453
/*tag= ab
/product= CFTR
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/product= pVIII protein
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             /number = 2
/note= "33K protein"
/a1379. 14526
/*tag= //faction |
14547. 16304
/*tag= | Protein |
14547. 16304
/*tag= | Peripentonal hexon-associated protein |
/note= | Peripentonal hexon-associated protein |
/note= | Major late mRNA L1 poly A signal (putative) |
//a190. 18105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //doce- "Represents residues 10676-34096 of Ad2-E4/ORF6" 35069. .35973
                                                                                      068003;
26-MAR-1996 (first entry)
Ad2/-ORF6/PGK-CFTR nucledtide sequence.
Ad2/-ORF6/PGK-CFTR nucledtide sequence.
Necombinant adenovirus; Ad2/CFTR-1; adenovirus 2 serotype; Ela; Elb;
viral replication; gene expression; gene therapy; cystic fibrosis;
cystic fibrosis transmembrane conductance regulator; CFTR;
promoter; B3; p19; MHC; class 1; viral latency; pulmonary airway; ds.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    core protein
                                                                                                                                                                                                                                       note= "virion component III"
8112. .18708
*tag= k
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note- "Precursor to major
8778. 19887
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/product= pV protein
/product= "minor core protein"
20188. 20193
/*tag= m
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product= Penton protein
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12915. .36335
/*tag= a
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28993. .29366
/*tag= f
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Q68003 standard; DNA; 36335 BP.
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NW Recomb
KW Promot Color Col
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The DNA construct comprises a full length copy of the Ad2 genome from which the early region I genes (EI genes) have been deleted and replaced by an expression cassette encoding CFTR. The expression cassette horludes the promoter for PGR and a poly-A addition signal from the Davine growth hormone gene. The Ad2-ORF6/PGR-CFTR construct differs from that given in Q68002 (Ad2/CFTR-I), in that the latter utilises the endogenous BIa promoter, has no poly-A addition signal directly be administered to the pulmonary airways in the gene therapy of cystic fibrosis. 88888888888888

9786 G; 10000 C; 8597 A; 36335 BP; Sequence

0; Gaps Query Match

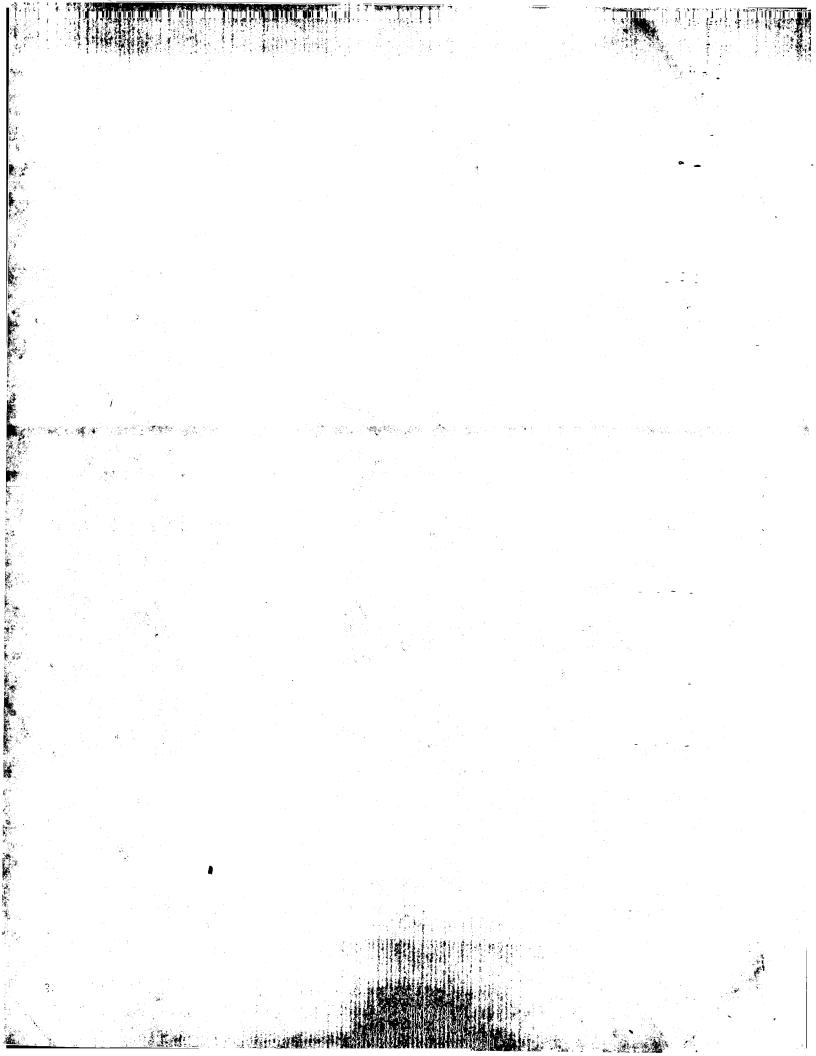
98.9%; Score 875.4; DB 1; Length 36335;
Best Local Similarity 99.3%; Pred. No. 2.3e-265;
Matches 879; Conservative 0; Mismatches 6; Indels 0; à 셤 ò ద à 셤 å 셤 å ద à g à 쉱

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Search completed: June 23, 2000, 10:05:42 Job time: 3610 sec



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Best Local Similarity 100.0%; Pred. No. 3.36-282;
Matches 885; Conservative 0; Mismatches 0; Indels
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-735-609-4
US-08-735-609-1
US-08-735-609-1
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US-08-151-391A-1
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US-08-151-391A-1
US-08-151-391A-1
US-08-151-391A-1
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US-08-101-1
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US-08-187-785-1

PCT-0853-0551-28

US-08-591-492-16

US-08-43-979A-20

US-08-43-979A-20

US-08-43-97-20

US-08-49-995-3

PCT-US91-0225-9

US-07-681-7038-1

US-07-681-7038-1

US-08-184-236-1

US-08-184-236-1
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ALIGNMENTS

Viruses for Gene Therapy 9 457	Length 8299;
M. M. na J. na J. od for Improved Production of for Improved Production Howson corporate Cntr., P.O. Box tible OS/MS-DOS lease #1.0, Version #1.30 syssyssyssyssyssyssyssyssyssyssyssyssy	100.0%; Score 885; DB 2; 100.0%; Pred, No. 3.3e-282;
RESULT 1 10S-04-462-014-2 10S-04-462-014-2 Sequence 2, Application US/08462014 Sequence 2, Application US/08462014 Sequence 2, Application US/08462014 Patent No. 5756283 GENERAL INFORMATION: Method for TITLE OF INVENTION: Method for CITY: Spring House Corporate STATE: PA COMPUTER: PA ZIP: 14477 COMPUTER: IBM PC COMPATIBLE OF STATE: PATENTION HOUSE COMPUTER: IBM PC COMPATIBLE OF STATE: PATENTION NUMBER: US/08/46: FILLING DATE: OS-TUN-1995 CLASSIFICATION NUMBER: US/08/46: ATTORNEY/AGENT INFORMATION: TELECOMMUNICATION NUMBER: 31,215 REGISTRATION NUMBER: 31,215 REFERENCE/POCKET NUMBER: UFNITELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMUNICATION INFORMATION: TELECOMMUNICATION INFORMATIO	Query Match

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Retent No. 5555360
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Manalfitano, Andrea
APPLICANT: Manalfitano, Andrea
APPLICANT: Munar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
INVERS OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
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US-08-735-609-4/c
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100.0%; Score 885; DB 4; L. Best Local Similarity 100.0%; Pred. No. 7.1e-282; Matches 885; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                      #1.30
         Suite 2200
                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elba PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
FILING DATE:
CLASSIFICATION: 435
ATTONREY AGENT INFORMATION:
NAME: Ligolia, Diane E.
REGISTRATION NUMBER: UM-02484
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION SEQ. ID NO: 4:
SEQUENCE: (415) 397-8338
INFORMATION FOR SEQ. ID NO: 4:
FURNICHED: AND THE SETIESTICS:
FURNICHED: AND THE
                                                                                           United States Of America
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
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TYPE: nucleic acid
STRANDEDNESS: double
220 Montgomery
                            CITY: San Francisco
STATE: California
COUNTRY: United Stat
ZIP: 94104
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                                                         gtccccgccatgagctttggatacagcgccttgcactgtgggattttgaagaatattgtg
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SOFTWARE: PATENTIN Release #1.0, Version #1.25
"CURREMY APPLICATION DATA:
"APPLICATION NUMBER: US/08/374,483
"CLASSTEPARTS: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE.

CLASSIFICATION:
ATTORNEY/GENT INFORMATION:
NAME: WILSON, MARY J.
NAME: WILSON, MARY J.
RESISTRATION NUMBER: 1579-83
REFERENCE/DOCKET NUMBER: 1579-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: GEORGE, SAMUEL E.
APPLICANT: BLAZING, MICHAEL A.
TITLE OF INVENTION: ADENOVIRAL VECTOR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSE: NATION & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
SOFTWARE: PatentIn Release #1
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
105-08-374-483-6/c
56quence 6, Application US/08374483
7, Patent No. 5880102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-374-483-6
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nucleic acid
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SEQUENCE CHARACTERISTICS
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Gaps

100.0%; Score 885; DB 3; Length 34382; 100.0%; Pred. No. 7.1e-282; .ive 0; Mismatches 0; Indels 0;

Query Match Best Local Similarity 100.0 Matches 885; Conservative

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31558 AGGACAAGGCGCCTTATGCTGCGGGCGGTGCGAATCATCGCTGAGGAGACCACTGCCATG 31499
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                                                            atactggaggatcatccgctgctgccgaatgtaacactttgacaatgcacaacgtgagt 180
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APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
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Patent No. 5955360
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US-08-735-609-1/c
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33297 TIGIATICCIGCAGGACGGAGCGGCGGCGCAGCAGTITATICGCGGCCCTGCTGCAGCAC 33238
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                                                                                                                                   gtccccgccatgagctttggatacagcgccttgcactgtgggattttgaadaatattgtg
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APPLICANT: MEHTALI, Majid
APPLICANT: PAVIRANI, Andrea
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
TITLE OF INVENTION: COMPLEMENTATION LINES
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2IP: 2314-276
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/379,452
FILING DATE: 26-JAN-1995
CLASSIFICATION NUMBER: WO PCT/FR94/00624
FILING DATE: 27-MAY-1994
PRIOR APPLICATION NUMBER: WO PCT/FR94/00624
FILING DATE: 27-MAY-1994
PRIOR APPLICATION NUMBER: FR 93 06482
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: #40,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: BURNS, DOANE, SWECKER & MATHIS, L.L.P. 1737 King Street, Suite 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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US-08-379-452-43
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DO
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Best Local Similarity
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US-08-379-452-43/c
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                                                                                                                                                         COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
: 220 Montgomery Street, Suite 2200
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Ingolia, Diame E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 397-838
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER/STICS:
                                                              California
: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
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TYPE: nucleic acid
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                                                                 STATE: C. COUNTRY:
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32733 CAGCGCTTCCCCTGGTACCCCAGATTGTAACAGAACATGCCCAAAGAGATCATGTAT 32674
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CORRESPONDENCE ADDRESS:
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US-08-752-760A-1
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                    1 atgactacgtccggcgttccatttggcatgacactacgaccaccacagatctcggttgtct
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APPLICANT: Gregory, Richard J.
APPLICANT: Smith, Alan E.
TITLE OF INVENTION: CHIMERIC ADENOVIRAL VECTORS
NUMBER OF SEQUENCES: 3
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Patent No. 5877011
GENERAL INFORMATION:
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       Conservative
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US-08-752-760A-1/c
       Matches 885;
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32853 GGGTACGAGCGCTGGATCCTGCATTGCCACTGTTCATCCCCTGGCTCCCTGCAGTGTCGG 32794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 ggttacgagtcctgggctctccactgtcattgttccagtcccggttccatgcagtgtata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 gccggcgggcaggttttggccagctggtttaggatggtggtggatggcgccatgtttaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32913 TGTATGTCAGTGTGCCTGTGCCCCGCTACCCTGGACTTGGTAAGAGCTCAGATGGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 atgcacaacgtgagttacgtgcgaggtcttccctgcagtgtgggatttadgctgattcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaaaccgcgctaccatactggaggatcatccgctgctgccgaatgtaacactttgaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 35081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 319.2; DB 3;
Pred. No. 5.7e-95;
0; Mismatches 308;
                                                                                                                                                           MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
SOFTWARE: FastESD Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,760A
FILING DATE: NOVV-1996
CLASSIFICATION NUMBER: APPLICATION NUMBER: Selde, Rochelle K
REGISTRATION NUMBER: 32,300
REFERENCE/POCKET NUMBER: 32,300
REFERENCE/POCKET NUMBER: 32,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION TELEPHONE: 212-705-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.1%;
Best Local Similarity 62.4%;
Matches 520; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35081 base pairs
TYPE: nucleic acid
ADDRESSEE: Baker & Botts, STREET: 30 Rockefeller Pi CITY: New York STATE: NY COUNTRY: U.S.A. ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-705-5020
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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715 gocoggagacaaggogcottatgotgogggoggtgogaatcatogotgaggagaccact 774
                                                                                                                                                                                                                                                                                                                              775 gccatgitgtaticctgcaggacggagcggcggcggcagcagtttaticgcgcgctgctg 834
                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 49.7%; Pred. No. 0.15;
Matches 85; Conservative 0; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     835 cagcaccaccgccctatcctgatgcacgattatgactctacccccatgtag 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 GIAAACGIGCIGCICTACGACATGAACGGCIGTIACICACGCCICAAGGAG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DUDS/MS-DUDS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,391A
FILING DATE: 12-NOV-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mills, Demetra J.
REGISTRATION NUMBER: 715-087
FELEPANCE/DOCKET NUMBER: 715-087
TELEPANCE/DOCKET NUMBER: 715-087
TELEPANCE, (703)684-1111
TELEPAN: (703)684-1124
TELEX: 82-4425
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 509 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: LOWE, PATCE, LEBLANC & BECKER STREET: 99 Canal Center Plaza, Suite 300 CITY: Alexandria STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Oda, Kinichiro
APPLICANT: Nakada, Susumu
APPLICANT: Hara, Eiji
APPLICANT: Yamaguchi, Tomoko
APPLICANT: Nakamura, Takeshi
APPLICANT: Oka, Yumiko
APPLICANT: Oka, Yumiko
APPLICANT: Kishimoto, Toshihiko
TITLE OF INTENTION: Human ID Genes
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                               ; LOCATION: 22..465
; OTHER INFORMATION: /note= "CDS"
US-08-151-391A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-151-391A-1
; Sequence 1, Application US/08151391A
; Patent No. 5527897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                            706 egetgetgtgeceggaggagaaaggegecttatgetgegggeggtgegaateategetgag 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
COUNTRY: U.S.A.
ZIP: 2314
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN DATA:
COMPUTER: LANOV-1993
CONFURENT APPLICATION DATA:
PPLICATION NUMBER: US/08/151,391A
FILING DATE: 12.NOV-1993
CLASSIFICATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 34,506
TELEFRAN: (703)684-1111
TELEFRAN: (703)684-1124
TELEFRAN: (703)684-1124
TELEFRAN: (703)684-1124
TELEFRAN: (703)684-1124
TTELEFRAN: (703)684-1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATENT NO. 5527897

GENERAL INFORMATION:
APPLICANT: Oda, Kinichiro
APPLICANT: Nakada, Susumu
APPLICANT: Hara, Elji
APPLICANT: Hara, Elji
APPLICANT: Nakamura, Takeshi
APPLICANT: Oka, Yumiko
TITLE OF INVENTION: Human ID Genes
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
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Length 1391;

48; Indels

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259 cgggaggagcttgtaatcctgaggaagtgtatgcacgtgtgcctgtgttgtgccaacatt 318
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                                                                                                                                                                                                                                                                                               3.6%; Score 32.2; DB 4;
56.0%; Pred. No. 0.63;
tive 0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)-546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 546-9392
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7326 base pairs
      3.6%
Best Local Similarity 56.0%
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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US-08-194-468-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     835 cagcaccaccgccctatcctgatgcacgattatgactctacccccatgtag 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 GIAAACGIGCICIACGACAIGAACGCIGIIACICACGCCICAAGGAG 252
                                                                                                                                                                   Length 509;
                                                                                                                                                         Query Match
3.8%; Score 33.4; DB 1;
Best Local Similarity 49.7%; Pred. No. 0.15;
Matches 85; Conservative 0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPÉTILLE
COMPUTER: IBM COMPÉTILLE
COMPUTER: IBM COMPÉTILLE
OPERATIOS SYSTEM: DOS
SOFTWARE: FRASEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,336
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY, AGENT INFORMATION:
NAME: BAILLINGS, LUCY J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Noanne R.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: NEW HUMAN DP1 HOMOLOG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: A
; LOCATION: 22..483
; OTHER INFORMATION: /note= "CDS"
US-08-151-391A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-865-336-2/c
; Sequence 2, Application US/08865336
; Patent No. 5958725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRACTERISTICS:
LENGTH: 1391 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SINTNOT02
CLONE: 236773
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US-08-194-468-1/c

Sequence 1, Application US/08194468

Sequence 1, Application US/08194468

Sequence 1, Application US/08194468

Sequence 1, Application US/08194468

Sequence 1, Application US/08346

Sequence 1, Application US/08346

PAPLICANT: Montminy, Marc R.

TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN TITLE OF INVENTION RESPONSIVE GENES

NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6296 GCCATTAGCTGTGGGTTTGATTTAAGGATGTTCAGCACCTGCTGCTGCTGAGGAGAG 6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       628 gccttgcactgtgggattttgaacaatattgtggtgctgtgctgcagttactgtgctgat 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 688 ttaagtgagatcagggtgcgctgctgtgcccggaggacaaggcgccttatgctgcgg 744
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                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: Pretty, Schroeder, Brueggemann & Clark
STRET: 444 South Flower Street, Suite 2000
STRIT: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE STATEM FOLOS/MR. 1.25
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,468
FILING DATE: 10-FEB-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Relier, Stephen E.
REGISTRATION NUMBER: 31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.5%
Query Match
Best Local Similarity 53.8%
Matches 63; Conservative
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US-08-865-336-2

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NUCLEOTIDE SEQUENCE AND A METHOD FOR.
                                                                                                                                                            2516 CCTCATTTGGAACGGAGATCGCGTCTTTATTGACAGGTGGTGCTACCAACCCAATGTGCTCGAA 2575
                                                 91 cotcottttgagacagaaacccgcgctaccatactggaggatcatccgctgctgccgaa 150
84; Indels
                                                                                                                                                                                                                                                                                                                                 2636 GCAATGCCGCACTGATACAGGAGTGGACACCCGAATCTGGTACCA 2680
                                                                                                                                                                                                                                                                             211 tttacgctgattcaggaatgggttgttccctgggatatggttcta 255
                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08905817

Sequence 1, Application US/08905817

Patent No. 582477;

Patent No. 582477;

APPLICANT: SASAKI, Keiko

APPLICANT: MORI, Takayuki

TITLE OF INVENTION: ATTENDATED MEASLES VIRUS VACCII

TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON

STREET: 745 South 23rd Street

CITY: Arlington

STATE: VISHING

ZIP: ACCOUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15894 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15894 base pal
81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid STRANDEDNESS: single
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1807..3327
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MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
Matches
                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE AND A METHOD FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 15894;
                                                                                                                         GENERAL INFORMATION:
APPLICANT: SASAKI, Keiko
APPLICANT: SASAKI, Takayuki
APPLICANT: MORI, Takayuki
APPLICANT: MORI, Takayuki
APPLICANT: MORI, Takayuki
TITLE OF INVENTION: CONTAINING SPECIFIC NUCLEOTIDE SEQUE
TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STREET: Virginia
CONTEX: USA
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SURFARE: Patentin Release #1.0, Version #1.30
SUFFRARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US /08/348,891A
FILING DATE: 15-NOV-1994
CLISSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,400
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 3-293625
FILING DATE: 14-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/COKET NUMBER: RP-7501
TELECOMMUTCATION:
TELECHONE: 708-521-2297
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Pred. No. 8;
                                                                        Sequence 1, Application US/08348891A Patent No. 5654136
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TELEX: 248425 EMBON
INFORMATION FOR SEQ ID MO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 15894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
3438..4442
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9234..15782
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1807..3327
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5458..7107
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108..1682
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Best Local Similarity
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LOCATION:
FEATURE:
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LOCATION:
FEATURE:
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LOCATION:
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LOCATION:
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259 cgggaggagcttgtaatcctgaggaagtgtatgcacgtgtgcctgtgttgtgccaacatt 318
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Best Local Similarity 53.3%; Pred. No. 4.4;
Matches 64; Conservative 0; Mismatches 56; Indels 0;
                                                                                                             Length 972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1. Application PC/TUS9508354A
GENERAL INFORMATION:
APPLICANT: Temple University - Of The
APPLICANT: Commonwealth System of Higher Education
TITLE OF INVENTION: JAK3 PROTEIN TYROSINE
TITLE OF INVENTION: KINASE AND DNA ENCODING THE SAME
TITLE OF INVENTION: KINASE AND DNA ENCODING THE SAME
TITLE OF INVENTION: KINASE AND DNA ENCODING THE SAME
TITLE OF INVENTION: GOIDA, LAVORING
CORRESPONDENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: 6 Monaco, P.C.
STREET: Suite 1800, Two Penn Center
CITY: Philadelphia
                                                                                                        Score 30.4; DB 6; Length 9 Pred. No. 2; 0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: PCT/US95/08354A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/272,368
FILING DATE: 8 July 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MODACO, Daniel A. REGISTRATION NUMBER: 30,480 REFERENCE/DOCKET NUMBER: 605 TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-8383
                                                                                                                  Query Match
Best Local Similarity 53.33
Matches 64; Conservative
            MOLECULE TYPE: CDNA PCT-US95-04801-2
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Best Local Similarity 49.1%; Pred. No. 8;
Matches 81; Conservative 0; Mismatches 84; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Martin, Juan F.
APPLICANT: Martin, Juan F.
APPLICANT: Coque, Juan R.
APPLICANT: Enguite, Francisco J.
APPLICANT: Liaren, Francisco J.
APPLICANT: BOUNTESSEE: John W. Wallen III
STREET: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2636 GCAATGCCGCACTGATACAGGAGTGGACACCCGAATCTGGTACCA 2680
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04801
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ATTORNEY/AGENT INFORMATION:
NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 191
TELECOMMUNICATION INFORMATION:
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9234..15<u>7</u>82
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7271..9121
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5458..7107
                         CDS
3438..4442
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LOCATION:
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FEATURE:
LOCATION:
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US-08-905-817-1
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2244 GATCTTGGTAAAAGAACCGTGACCCAGGTTCTCGTGTCCCAGGCTGTCCGTTGGAATTGT 2185
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                                                                                                                                                                                                      Sequence 1, Application US/08982956
Fatent No. 3861312
GENERAL INFORMATION:
APPLICANT: Varshavsky, Alexander
APPLICANT: KWON, YONG Tae
TITLE OF INVENTION: NUCLEIC ACID ENCODING MAMMALIAN UBRI
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STATE: ME
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/982,956
FILING DATE:
FI
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3.4%; Score 30.4; DB 3; Length 6395;
Best Local Similarity 57.3%; Pred. No. 5.7;
Matches 55; Conservative 0; Mismatches 41; Indels 0
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 55,505
REFERENCE/DOCKET NUMBER: CIT-2001
TELECOMMUNICATION INFORMATION:
TELEFRAX: (207) 363-0558
INFORMATION FOR SEQ ID NO: 1:
'SEQUENCE CHARACTERISTICS:
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LOCATION: 115..5385
US-08-982-956-1
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MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                            RESULT 15.
US-08-982-956-1
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Search completed: June 23, 2000, 09:51:07 Job time: 6653 sec

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em_est30:
gb_est40:
gb_est40:
gb_est41:
gb_est41:
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em_est31:
em_est32:
em_est33:
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em_est22:
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em_est24:
em_est24:
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gb_est33:
gb_est34:
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                                                                                                                                                                                   June 23, 2000, 05:42:32; Search time 592.38 Seconds (without alignments) 6055.408 Million cell updates/sec
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885
1 atgactacgtccggcgttcc.....atgactctaccccatgtag 885
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                                      GenCore version 4.5
Copyrigims (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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Trotal number of hits satisfying classify and the sequents of the satisfying classify and the sequents of the seq
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Perfect score:
Sequence:
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Email: Robert Strausberg@nih.gov	e Procurement el R. Emmert- Library Prep Library Arra Sequencing by e distributio through the	Possible reversed clone: polyT not found Seq primer: -40UP from Gibco High quality sequence stop: 438. EATURES Location/Qualiflers source 1.0.564	/Organism="Homo sapiens" /db_xref="taxon:9606" /clone="InAGE:2746581" /clone=lib="NCI_CGAP_Ov40" /sex="female"	ovarian metastasis" : pAWP10; cDNA made by oligo cloned into the UDG sites o garcos gel, average insert try; non-amplified chua	Library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383." BASE COUNT 158 a 175 c 117 g 112 t 2 others ORIGIN	Query Match 58.9%; Score 521; DB 79; Length 564; Best Local Similarity 98.7%; Pred. No. 3.3e-147; Matches 524; Conservative 0; Mismatches 7; Indels 0; Gaps	121 atactggagatcatccgctgctgcccgaatgtaacactttgacaatgcacaacgtgagt 180 	181 tacqtqcqagqtcttccctqcagtqtqgqatttacqctqattcagqaatgqqttqttccc 240 	241 tgggatatggttctaacgcgggaggagcttgtaatcctgaggaagtgtatgcacgtgtgc 300 	301 ctgfgttgfgccaacattgatatcatgacgagcatgatgatccatggttacgagtcctgg 360 	361 getetecaetgteattgttecagteceggttecetgcagtgtatageeggegggaggtt 420 	421 ttggccagctggtttaggatggtggtggatggccatgtttaatcagaggtttatatgg 480 	481 taccgggaggtggtgaattacaacatgccaaaagaggtaatgtttatgtccagcgtgttt 540 ,	541 atgagggtcgccacttaatctacctgcgcttgtggtatgatggccacgtgggttctgtg 600 	601 gtcccgccatgagctttggatacagcgccttgcactgtgggattttgaac 651
		FEA			BASE	O Be Ma	S S	Q Q	0 <u>y</u>	oy Og	Oy Op	Oy Op	දු පු	Qy Dp	Oy Db
Description	AW265091 AW277220 AW277220 XG79D06.x AW277227 AW277220 XG70B00.x AW419027 AW419027 AW419027 XG4504.x AW419099 AW438779 AW438779 XG50609.x AW55034 AM5509 AW56009.x AM55034 AM5610.s AM5649817 ns48801.s									ALIGNMENTS	564 bp mRNA EST 28-DEC-1999 NCI_CGAP_OV40 Homo sapiens cDNA clone IMAGE:2746581 3' SW:E434_ADE02 P03239 EARLY E4 34 KD PROTEIN. ;, mRNA		Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.	NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	ence version replaced g1:5406367.
core Match Length DB ID	521 58.9 564 79 72 228.6 25.8 515 79 72 228.6 25.8 515 81 228.6 25.8 515 81 228.6 25.8 516 81 2213.2 24.1 429 36 72 22.8 22.8 30.1 36 72 22.8 30.1 30 72 22.8 30.1 30 72 22.8 30.1 30 72 22.8	22.0 445 36 22.0 445 36 4.9 630 79 4.8 922 82 4.6 848 82 4.5 393 109	4.4 1101 82 4.4 1101 83 4.3 1101 83 4.3 424 100	4.2 537 927 4.2 544 92 4.1 511 91 4.0 939 82 4.0 681 91	4.0 827 84 4.0 1101 83 3.9 434 48 3.9 442 109	3.9 380 41 3.9 1101 82 3.9 400 31 3.8 600 106	3.8 791 60 3.8 1101 82 3.8 339 22 3.8 415 33	3.8 429 34 3.8 1101 83 3.8 511 23 3.8 536 63	3.8 436 61	í.		Sequence. AW265091 AW265091.1 GI:6641907 BST.	Homens Sapiens Eukaryota; Metazoa; Chor Eutheria; Primates; Cata	NCI-CGAP http://www.ncbi National Cancer Institut Tumor Gene Index	Unpublished (1997) On Jul 7, 1999 this sequence version replaced Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
No. S	00 100400 000000	0 11110	0 11 12 12 13 14 15 15 15 15 15 15 15 15 15 15 15 15 15	21 21 22 22 23 24 25	27 27 27 27 27 29 20 20 20 20 20 20 20 20 20 20 20 20 20	3333	, o o o o o o o o o o o o o o o o o o o	D	* 4 * 33 * 4	RESULT 1	AWZ65U9I/C LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	ORGANISM	AUTHORS	COMMENT

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711 ctgtgcccggaggacaaggcgccttatgctgcgggcggtgcgaatcatcgctgaggagac 770
1 .515

/organism-"Homo sapiens"

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/lab_host="DH108"
                                                                                                                                                                         AW277227
AW277227.1 GI:6664257
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Matches 231; Conserv
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priming. Non-directionally cloned into the UDG sites of
pAMP10. Size-selected on agarose gel, average insert
size 500 bp. Primary library; non-amplified. cDNA
Library Preparation: David B. Krizman, Ph.D (NCI).
                                      AW277220 612 bp mRNA EST 03-JAN-2000 xq79b06.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756819 3' similar to SW:E434_ADE02 P03239 EARLY E4 34 KD PROTEIN. ; mRNA
                                                                                                                                                            Homo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 612)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAIIONAI Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                               Tumor Gene Index
Tumor Gene Index
Unpublished (1997)
On May 18, 1998 this sequence version replaced gi.3137497.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Enail: Robert_Strausberg@nih.gov
Unknown library type
Possible reversed clone: polyT not found
Seq primer: 400P from Gibco
High quality sequence stop: 375.
High quality sequence stop: 375.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 56.8%; Score 503; DB 79; Length 6: Best Local Similarity 91.5%; Pred. No. 9.9e-142; Matches 530; Conservative 0; Mismatches 49; Indels
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/clone-"IMAGE:2756819"
/clone_llb-"NCI_CGAP_Lu34"
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                                                                                            sequence.
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AW277220.1 GI:6664250
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                       RESULT 2
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SM Homo sapiens
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Primates; Catarrhini; Hominidae: Homo.
Eutheria: Primates; Catarrhini; Hominidae: Homo.
Eutheria: Primates; Catarrhini; Hominidae: Homo.
Eutheria: Primates; Catarrhini; Homon cancer
Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
On May 18, 1998 this sequence version replaced gi:3137504.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
unknown library type
Possible reversed clone: similarity on wrong strand
Possible reversed clone: similarity not found
Seq primer: -400F from Gibco
High quality sequence stop: 427.
High quality sequence stop: 427. /note="Organ: ling; Vector: pAMP10; cDNA made by oligo-dr priming. Non-directionally cloned into the UDG sites of priming. Size-selection agarose largery average insert pamp10. Size-selected on agarose largery size 500 bp. Primary library; non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383. AW277227 515 bp mRNA EST † 03-JAN-2000 xq80a02.xl NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756906 3' similar to SW:E417_ADE02 P03238 PROBABLE EARLY E4 17 KD PROTEIN. [COUPLINS: E4 10 KD PROTEIN]. ; mRNA sequence. 651 caatattgtggtgtgtgtgtgctgcagttactgtgctgatttaagtgagatcagggtgcgctg 710 25.8%; Score 228.6; DB 79; Length 515; llarity 98.3%; Pred. No. 1.3e-58; Conservative 0; Mismatches 4; Indels 0; Gaps gtgaattacaacatgccaaaagaggtaatgtttatgtccagcgtgtttatgaggggtcgc 552 5 ceacalicidesecretecrecretracretrereartraagreagarcagesere

LOCUS DEFINITION

RESULT AW419027

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL COMMENT

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin; Hominidae; Homo. p

Eutheria; Primates; Catarrhin; Hominidae; Homo. p

I (Dases 1 to 516)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

No Jan 6, 2000 this sequence version replaced gi:6677339.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausbergenih.gov

Contact: Robert Strausbergenih.gov

CONA Library Preparation: David B. Krizman, Ph.D.

CONA Library Preparation: David B. Krizman, Ph.D.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Mashington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW438779 516 bp mRNA EST 14-FEB-2000 xu38e04.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2803998 : similar to SW:E417_ADE02 P03238 PROBABLE EARLY E4 17 KD PROTEIN [CONTAINS: E4 10 KD PROTEIN].; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                              /note="Organ: lung; Vector: pAMP10; cDNA made by oligo priming. Non-directionally cloned into the UDG sites pAMP10. Size-selected on agarose gel, average insert Library Preparation: Primary library; non-amplified. cDNA Reference: Krizman et al. (1996) Cancer Research 56:5300-5383.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.8%; Score 228.6; DB 81; Length 516; 98.3%; Pred. No. 1.3e-58; iive 0; Mismatches 4; Indels 0;
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Location/Qualifiers
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/clone=lib="NGI_CGAP_Lu34"
/tissue_type="large cell carcinoma"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael Kelley M.D., John Gillespie M.D.,
Michael Emmert-Buck M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
Www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: lung, Vector: pAMP10; cDNA made by oligo-dr
priming. Non-directionally cloned into the UDG sites of
pAMP10. Size-selected on agarose gel, average insert size
500 bp. Primary library; non-amplified. cDNA Library
Preparation: David B. Krizman, Ph.D (NCI). Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."
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1 (bases 1 to 515)

NCI-GGAP http://www.ncbi.nim.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (GGAP), Tumor Gene Index

Unpublished (1997)

On Jun 22, 1998 this sequence version replaced g1:3247377.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@ilh.gov
                                                                                                                                                                                                                                                                                                         771 cactgccatgttgtattcctgcaggacggacggcggcggcggcagcagtttattcgcgcgct 830
                                                                                                                                                                                                            65 CIGIGCCCGGAGGACAAGGCGICICAIGCIGCGGGCGGIGCGAAICAICHIIIIIIIII
                                                                                                                                                                                                                                                                                                                                              Possible reversed clone: similarity on wrong strand Seq primer: -400P from Glbco High quality sequence stop: 425.
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/organism="Homo sapiens"

/db xref="taxon:9606"

/clong="IMAGE:2856127"

/clong="Lib="NGT_CGAP_Lu34.1"

/tissue_type="large cell carcinoma"

/lab_host="DH10B"
| Mon Jun 26 09:10:32 2000 | Mon Jun 26 09:10:32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW419027.1 GI:6946959
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Best Local Similarity 98.3%;
Matches 231; Conservative
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FEATURES

BASE COUNT ORIGIN

711 ctgtgccggaggacaaggcgccttatgctgcgggcggtgcgaatcatcgctgaggagac 770

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711 ctgtgcccggaggacaaggcgccttatgctgcgggcggtgcgaatcatcgctgaggagac 770

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

LOCUS

RESULT AW340909

JOURNAL ..

SCHOOL STATE COMMENT

REFERENCE AUTHORS TITLE

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Tunor Gene Index
I uppublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1288483.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 495-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed b
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Information can be
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 429)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Krizman et al.
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69 CCCGGAGGACAAGGCGTCTCATGCTGCTGCGGTGCGAATCATCGCTGACGAGACCACTG 128
                                                                                                                             129 ccargingraficcigcaggacgagcggcggcggcagcagrifaticgcgcgcrgcigc 188
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                                                                                                                                                                                                                              Score 213.2; DB 36; Length
Pred. No. 5.6e-54;
0; Mismatches 8; Indels
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/clone="IMAGE:1186897"
/clone="INCI_CGAP_Alv1"
/tissue_type="alveolar rhabdomyosarcoma"
/lab_host="DH108"
                                                                                                                                                                                                  agcaccaccgccctatcctgatgcacgattatgactctacccccatgtag
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High quality sequence stop: 404.
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/organism="Homo sapiens"
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llarity 96.2%;
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/db_xref="taxon:9506"
/db_xref="taxon:9506"
/clone="IxAGE:285661"
/clone="laye="large cell carcinoma"
/tab_host="large cell carcinoma"
/lab_host="DH10B"
/note="organ: lung; vector: pAMP10; cDNA made by oligo-dT priming. Non-directionally cloned into the UDG sites of paMP10. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. cDNB Library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
83 a 110 c 118 g 92 t
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Coppublished (1997)
On May 18, 1998 this sequence version replaced gi:3137759.
On May 18, 1998 this sequence version replaced gi:3137759.
Contact: Robert Strausberg@nih.gov
Tissue Procurement: Michael Relley M.D., John Gillespie M.D.,
Michael Emmert-Buck M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium(LINL)
Clone distribution: NGI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                        AW340909 403 bp mRNA EST 31-JAN-2000 xy50e09.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856616 3' similar to SW:E434_ADE02 P03239 EARLY E4 34 KD PROTEIN: ;, mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 403)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/nciogap.
NAI-CGAP http://www.ncbi.nlm.nlh.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AW340909.1 GI:6837535
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center-
Clone distribution: NI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D. Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 301)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                          301 bp mRNA EST 13-NOV-1997 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1186873 SW:E434_ADE02 P03239 EARLY E4 34 KD PROTEIN. ;, mRNA
97 CIGIGCCGGA-GACAAGGCGTCTCAIGCTGCGGGCGGTGCGAATCATCGCTGAGGAAC 155
                                                                                      113 SCTGCTGCAGCACCACCGCCCTATCCTGATGCACTATATGACTCTACCCCCATGTAG 270
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Non-directionally cloned. Size-selected on agarose average insert size 600 bp. Reference: Krizman et (1996) Cancer Research 56:380-5383."
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                                                                  828 getgetgeageaceacegecetatectgatgeacgattatgactetaceceatgtag
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Unpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:430266.
Contact Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@aih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:1186873"
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/tissue_type="alveolar rhabdomyosarcoma"
/lab_host="bH10B"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                          sequence.
AA649817
AA649817.1 GI:2577145
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Matches 227; Conservative
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similar to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: colon; Vector: pAMPIO; cDNA made by oligo-d
priming. Non-directionally cloned into the UDG sites of
pAMPIO. Size-selected on agarose gel, average insert
size 500 bp. Primary library; non-amplified. cDNA
Library Preparation: David B. Krizman, Ph.D (NCI).
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 223)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tunor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3189136.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
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/db_xref="taxon:9606"
/clone="IMAGE:1754621"
/clone_lib="NCI_CGAP_CO22"
/tissue_type="colonic adenocarcinoma"
/lab_host="DH108"
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REFERENCE AUTHORS TITLE

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Tumor Gene Index
Inpublished (1997)
On Nov 22, 1999 this sequence version replaced gi:6462296.
On Nov 22, 1999 this sequence version replaced gi:6462296.
On Nov 22, 1999 this sequence Ph.D.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-11550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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priming. Non-directionally cloned into the UDG sites of
pAMPIO. Size-selected on agarose gel, average insert
size 500 bp. Primary library; non-amplified. cDNA
Library Preparation: David B. Krizman, Ph.D (NCI).
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383.
                                          AW276836 630 bp mRNA EST 03-JAN-2000 xp66911.x1 NCI_CGAP_Ov39 Homo saptens cDNA clone IMAGE:2745380 3' similar to SW:E413_ADE02 P03240 PROBABLE EARLY E4 13 KD PROTEIN. ;;
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AL066784
AL066784.1 GI:4945247
                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea to 630)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Possible reversed clone: similarity on wrong strend possible reversed clone: polyT not found seq primer: -40TP from Gibco High quality sequence stop: 422.

Location/Qualifiers

1. 630
/organism="Homo saplens"
/db_xref="texon:9606"
/clone="IMAGE:2745380"
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/sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. Days Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                      *AA642819 445 bp mRNA EST 27-OCT-1997 nu05b06.81 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1207091 .similar to SW:E417_ADE02 P03238 PROBABLE EARLY E4 17 KD PROTEIN ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                        /note="Vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma, cDNA made by oligo-dr priming.
Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cactgccatgttgtattcctgcaggacggaggcggcggcggcagcagtttattcgcgcgct 830
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22.0%; Score 194.6; DB 36; Length 445;
Best Local Similarity 94.9%; Pred. No. 2.5e-48;
Matches 223; Conservative 0; Mismatches 9; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 339.
Location/Qualiflers
1. .45
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMASE:1207091"
/tlssue_type="alveolar rhabdomyosarcoma"
/lab_host="lubing"
181 CCACCGCCCTATCCTGATGCACGATTATGACTCTACCCCCATG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             www-bio.lln1.gov/bbrp/image/image.html
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Gaps

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**Submitted (02-JUN-199) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web. in www.genoscope.cns.fr : segref@genoscope.cns.fr - Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster agenome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 150genic strain v2: no bw sp., the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
                                                                                          Drosophija melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
Genoscope.
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927P1-4G2.TP 927P1 Trypanosoma brucei genomic clone 927P1-4G2,
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastide; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/db_xxef="texon:7227"
/clone_lib="RPCI-98"
/clone="BACR34B02",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70;
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22.6%; Pred. No. 0.18;
tive 74; Mismatches 70;
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                                             GI:4952523
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AL072642.1
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Matches 42; Conserv
                                                                         fruit fly
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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR34B02 of ReCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Perryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Eplydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 922)
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4.8%; Score 42.2; DB 82;
Best Local Similarity 16.9%; Pred. No. 0.055;
Matches 60; Conservative 132; Mismatches 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila ;/db_xref="taxon:7227" /clone_lib="RPCI-98" /clone="BACR14D09"
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                                                                                                                                                Direct Submission
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RESULT 13 CNSOGWQ/c LCCUS DEFINITION

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Direct Submission

Ly Submitted (11-10W-1999) Genoscope - Centre National de Sequencagé : ..., submitted (11-10W-1999) Genoscope - Centre National de Sequencagé : ..., BP 191 91006 EVRY cedex - FRANCE (E-mail : Seqref@genoscope.cns.fr.

- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Obetermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila DRACOM Mammoser in Pieter de Jong slaboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, Cancer Genetics at the Roswall Park Cancer Institute in Buffalo.

NY. The library is named RPCI-98 and was constructed by partial Ecogn digestion of Drosophila DNA provided by the BDGP from the Ecog digestion of Drosophila DNA provided by the BDGP from the library pland EST libraries. A more detailed description of the library pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library. The found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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     1 (bases 1 to 393)
El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujli, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Dobelson, J., Fraser, C. and Adams, M.
Determination of clone end sequences from Trypanosoma brucel TREU 927/4 Pl library
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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                L Unpublished (1999)

L Unpublished (1999)

On Mar 23, 1999 this sequence version replaced gi:3323624.

On Mar 23, 1999 this sequence version replaced gi:3323624.

Other_GSSS: 927P1-462.TV

Context: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0208

Email: nelsayed@tigr.org

For clone/filter availability, please contact Sara Melville

For clone/filter availability, Please contact Sara Melville

(smic0@mole.bio.cam.ac.uk). Plead sequences search page:

http://www.tigr.org/tdb/mdb/tbdb/.
Seq Primer: SP6
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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RESULT 15 CNSOOLT2 LOCUS DEFINITION

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•	Page 1				d by chance to have a the result being printed, re distribution.			Description A52460 Sequence 4	M73260 Mastadenovi J01917 Adenovirus AR009152 Sequence	AF108105 Human adea k51800 Adenowirus 119443 Human achrom 104964 Human stero 104964 Human stero 104964 Human stero 10406187 Homo sapi 1068073247 Homo sapi 10680732 Arabidops 106813 Homo sapi 106813 Human chrom 10408543 Homo sapi 106814 Homo sapi 106814 Human sapi 10691814 Humo sapi 106814 Human sapi 106911 Synechocyst 10601535 Homo sapi 1068151 Human NEI-10691 Human sapi 106911 Synechocyst 10601535 Homo sapi 1068151 Human NEI-10691 Human sapi 1048151 Human NEI-11081 Human sapi 1048151 Human Sapi 1048151 Human Sapi 1048151 Human Sapi	
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GREYARK THTPYVPIDKEWKIEGFYMRMALKVLTLSDDLGYTRNBRIHKAVSVSRR
RELSDRELMHSLQRALGGTGSGDREAESYFDAGADLRWAPSRRALEAAGAGPGLAVAP
ARAGNVGGVEEYDEDDEYEPEDGEY
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RDSVSGLRVPvRTRPPRN"
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                                 /organism="Human adenovirus type/db_xref="taxon:28285"
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/protein_id-"AAA96410.1"
/db_xref-"GI:209847"
                                                                                                                                                                                                          /protein_id="AAA96406.1"
/db_xref="G1:209843"
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/product="protein pVII"
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Dedicu, J., Latta, M., Orsini, C., Perricaudet, M., Vigne, E. and Yeh, P. CELLS FOR THE PRODUCTION OF RECOMBINANT ADENOVIRUSES
Patent: WO 9622378 - A 25-JUL-1996;
Other publication RR 2729674 960726.

Cother publication FR 2729674 960726.

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/organism="unidentified"
/db_xref="taxon:32644"
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Best Local Similarity 100.0%; Pred. No. 5.5e-97;
Matches 345; Conservative 0; Mismatches 0;
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12 (bases 6039 to 6079; 7101 to 7172; 9634 to 9723; 18802 to 18861)
Akusjarvi, G. and Pettersson, U.
Sequence analysis of adenovirus DNA: complete nucleotide sequence.
of the spliced 5' noncoding region of adenovirus 2 hexon messenger
      weight ribonucleic acid
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Zain, B.S. and Roberts R.J.

Zain, B.S. and Roberts R.J.

Characterization and sequence analysis of a recombination site the hybrid virus Ad2+ND

The hybrid virus Ad2+ND

J. Mol. Biol. 120 (1), 13-31 (1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Akusjarvi,G. and Pettersson,U.
Nucleotide sequence at the junction between the coding region the adenovirus 2 haxon messenger RNA and its leader sequence Proc. Natl. Acad. Sci. U.S.A. 75 (12), 5822-5826 (1978)
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Akusjarvi,G. and Pettersson,U.
Sequence analysis of adenovirus DNA. I. Nucleotide sequence carboxy-terminal end of the gene for adenovirus type 2 hexon virology 91 (2), 477-480 (1978)
                                                                                                         Jornvall, H., Ohlsson, H. and Philipson, L.
An acetylated N-terminus of adenovirus type 2 hexon protein
Blochem. Blophys. Res. Commun. 56 (2), 304-310 (1974)
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Pan, J., Celma, M.L. and Weissman, S.W.

Studies of low molecular weight RNA from cells infected wit

Studies of low molecular weight RNA from cells the extension of the promoter for VA-RNA

J. Biol. Chem. 252 (24), 9047-9054 (1977)
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Shinagawa, M. and Padmanabhan, R.
Nucleotide sequence at the inverted terminal repetition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 (bases 1 to 156; 35804 to 35937)
Arrand,J.R. and Roberts,R.J.
The nucleotide sequences at the termini of adenovirus-2 i
The nucleotide sequences at (1979)
7. Mol. Biol. 128 (4), 577-594 (1979)
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                                                                                                                                                                                                                                                                                                                           Celma.M.L., Pan,J. and Weissman,S.M. Studdes of low molecular weight RNA from cells infected adenovirus 2. II. Reterogeneity at the 5' end of VA-RNA J. Blol. Chem. 252 (24), 9043-9046 (1977)
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Celma, M.L., Pan, J. and Weissman, S.M.
Studies of low molecular weight RNA from cells infected
adenovirus 2. I. The sequences at the 3' end of VA-RNA J
J. Biol. Chem. 252 (24), 9032-9042 (1977)
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21ff.E.B. and Evans, R.M.

Coincidence of the promoter and capped 5' terminus of adenovirus 2 major late transcription unit

Cell 15 (4), 1463-1475 (1978)
ine nucleotide sequence of a low molecular from cells infected with adenovirus 2 0. Biol. Chem. 246 (22), 6991-7009 (1971)
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Zain,S., Sa
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NSGAQLAGGFRHRVRSPGGGITHLITRGRGIQLANDESVSSSLGLRPDGTFQIGGAGRP
STPRRQALITLQISSSEPRSGGIGTLQFIEBEVPSVYFNPFSGPPGHYPDGFIPNEDA
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/prodect="protein pvIII"
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/translation="MSKEIPPPYMMSYOPOMGLAAGAAQDYSTRINYMSAGPHMISRV
/translation="MSKEIPPPYMMSYOPOMGLAAGAAQDYSTRINYMSAGPHMISRV
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/note="of a 33 K protein"
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Persson, H., Jornvall, H. and Zabielski, J.
Multiple mRNA species for the precursor to an adenovirus-encoded
glycoprotein: identification and structure of the signal sequence
Proc. Natl. Acad. Sci. U.S.A. 77 (11), 6349-6353 (1980)
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Anderson,C.W. and Lewis,J.B.
Amino-terminal sequence of adenovirus type 2 proteins: hexon, fiber, component IX, and early protein 1B-15K
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Nucleic Acids Res. 9 (1), 1-17 (1981)
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Osborne, T.F., Schell, R.E., Burch-Jaffe, E., Berget, S.J. and
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                                                                                                                                                                                                                                              27 (sites)
Van Etten,R.A., Walberg,M.W. and Clayton,D.A. 
Precise localization and nucleotide sequence of the two mitochondrial rRNA genes and three immediately adjacent
                               Natl. Acad. Sci. U.S.A. 77 (7), 3778-3782 (1980)
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Buttner,W and Veres-Wolnar,Z.
Localization of the 3'-terminal end of the EcoRI fragment-specific early mRNA of adenovirus type FEBS Lett. 122 (2), 317-321 (1980)
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Sequence 2 from patent US 5756283.
AR009152. GI:3967957
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Akusjarvi,G. and Pettersson,J.
Sequence analysis of adenovirus DNA. IV. The genomic sequences encoding the common tripartite leader of late adenovirus messenger
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Alestrom,P., Akusjarvi,G., Perricaudet,M., Mathews,M.B.,
Klessig,D.E. and Pettersson,U.
The gene for polypeptide IX of adenovirus type 2 and 1ts unspliced
messenger RNA
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Blogenesis, structures, and sites of encoding of the 5' termini of adenovirus-2 mRNAs
Cold Spring Harb. Symp. Quant. Biol. 44 PT 1', 415-428 (1980)
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Shinagawa,M., Padmanabhan,R.V. and Padmanabhan,R.
The nucleotide sequence of the right-hand terminal Smal-K fragment dency trus type 2 DNA
Gene 9 (1-2), 99-114 (1980)
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Perricaudet,M., Akusjarvi,G., Virtanen,A. and Pettersson,U.
Structure of two spliced mRNAs from the transforming region of human subgroup C adenoviruses
Nature 281 (5733), 694-696 (1979)
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Zain,S., Gingeras,T.R., Bullock,P., Wong,G. and Gelinas,R.E.
Determination and analysis of adenovirus-2 DNA sequences which include signals for late messenger RNA processing
J. Mol. Biol. 135 (2), 413-433 (1979)
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Baker,C.C., Herisse,J., Courtois,G., Galibert,F. and Ziff,E.
Messenger RNA for the Ad2 DNA binding protein: DNA sequences
Ceclin 18 (2), 569-580 (1979)
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Herisse,J., Courtois,G. and Galibert,F.

Nucleotide sequence of the EcoRI D fragment of adenovirus 2 in the EcoRI D fragment of adenovirus 
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Zain,B.S. and Roberts,R.J.
Sequences from the beginning of the fiber messenger RNA
adenovirus type 2 DNA
Biochem: Biophys. Res. Commun. 87 (3), 671-678 (1979)
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Structure of genes for virus-associated RNAI and RNAII
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Proc. Natl. Acad. Sci. U.S.A. 77 (5), 2424-2428 (1980)
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Predicted structure of two adenovirus tumor antigens
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Gallbert, F., Herisse, J. and Courtois, G.
Nuclectide sequence of the EcoRI-F fragment
Gene 6 (1), 1-22 (1979)
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Akusjarvi,G., Mathews,M.B., Andersson,P.,
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hlkvsvlvpfgrogfmalmdyhardiljosdvifagrroeltvllfnhtdrflyrk
ghpvgtllervifpsvkiaflv"
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Human adenovirus type 9

Viruses; daDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus

1 (bases 1 to 3119)

Javier,R, and Shenk,T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 atgactacgtccggcgttccatttggcatgacactacgaccaacacgatctcggttgtct 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammary tumors induced by human adenovirus type 9: a role for
                                                                                 | (bases 1 to 8299)
Wilson,J.M., Fisher,K.J. and Gao,G.
Welbod for improved production of recombinant adeno-associated
viruses for gene therapy
Patent: US 5756283-A 2 26-MAY-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SB2508 3119 bp DNA VRL 03-DEC-1996
984: orf2. ..orf7 [adenovirus type 9, Genomic, 6 genes, 3119
882508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Breast Cancer Res. Treat. 39 (1), 57-67 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
23.2%; Score 80; DB 5; L4
Best Local Similarity 100.0%; Pred. No. 2.4e-14;
Matches 80; Conservative 0; Mismatches 0;
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/gene="orf2"
/note="This sequence comes
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/db_xref="G1:1699392"
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1. .3119
                                                                                                                                                                                                                                                                          /organism="unknown"
2130 c 2108 g
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889
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                                  Unknown.
Unclassified.
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VERSION
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SOURCE
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AUTHORS
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AUTHORS
TITLE
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FEATURES
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RESULT S82508

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ORVLRDEDFEPNEQTGISPARAHVAAANLYTAYEQTYKQERNFQKSFNNHYRTLIARE
EVALGLMHLWDLAEAIVQNPDSKPLTAQLFLVVQHSRDNEAFREALLNIAEPEGKWLL
ELINILQSIVVQERGLSLAEKVAAINYSVLSLGKFYARKIYKTPYVPIDKEVKIDSFY
WRMALKVLTLSDDLGVYRNDRIHKAYSASRRRELSDRELMLSLRRALVGGAAGGEESY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FISALRIAVTEVPOSEVYOSGPDYFFOTSROGLOTVNLSOAFRNLRGLWGVOAPVGDR
STVSSLLTPNSRLLLLLIAPFTDSGSVNRNSYLGHLLTLYRBAIGQAOVDBOFFQEIT
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ATPSAALGNDTDSLRATINFLLTNROOKIPAOYALSABEBERILRYVQOSVGLFLMQEG
ATPSAALGNDTRNRNMEPSMY AANRPFINKLMYLHRAASMNSDYFTNALLNPHMTPPPG
FYTGEYDMPDPNDGFLWDDVDSAVFSPTLQRKOGAVRTPASEGGAVGRSPFPSGLASLHS
LEGSVNSGRYSRPRLLGEDEYLNDSLLQPPRVKNAMANNGIESLVDKLNRWKTYAQDH
REPAPAPRQRHDROOKLVWDDEDSADDSSVLDLGGSGGVNPISRILQPKLGRRMF"
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YNSTNYQSNLDRLYTDYREAVAQRERFKNEGLGSLVALNAFLATQPANVPRGQDDYTN
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SELAPLYDTTRYLVDNKSADIASLNYQNDHSNFLTTVVQNNDFTPARASTQTINFDE
RSRWGGDLATLLHFNMPNVPREVETSRRARVARRHPGOTVBATDLESKDILEYEWFE
FILDEGRFSETWILDLANNAILENTLOYGRQNGVLESDIGVREDSRNFKLGMDPVTKL
VMPGVYTYEAFHPDVVLLPGGGVDFTESRLSNILGIRKQPFOGGFRIWFEDGNFYRKL
PALLDVPRYKLESKKLEBERNARANGPARGDSSVSREVERAARELVIEDIKGDDT
KRSYNLIEGTMOTILTSKWYLSYTYRDPENGVGSWTLLTTPDVTGGAEQVTWSLPDDMO
DPVTFRSTQQVSNYPVVGAELMPRAKSFYNDLAVYSQLIRGYTSTHVVFNRFDNOIL
CORPAPPILTTVSENVPALTDHGTLPLRSSIRGVQRVTVTDARRRTCPYVYRALGIVA
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KNFGSTLRTYGNKAMSSTGQLLERELKDONFQGKVVDGLASGINGYVDIANGAVQRE
INSRLDPRPPTVVEMEDATLPPPRGEKRPREDAEETILQVDEPSYEEAVYRAGMPTTR
IIAPLATGVMKRATLDLPPPPPAPPRAAEVVQPPEPVATAVRRVPARRQAQNWQSTLH
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SANKLSLKVGHGLKILDDKSAGGLKDLIGKLVVLTGKGIGTENLONDGSSRGIGISV
RARBGLIFDNDGYLVVANNPKYDTRILMTTPDTSPNCRIDKEKDSKLTLVLTKGGSQIL
ANVSLIVVSGKYQYIDHATNPTLKSFKIKLLFDNKGVLLPSSNLDSTYWNFRSDNLTV
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AYSITFEFVWNKEYARVEFETTSFTFSYIAQQ"
                                                                                                                                                                               RLGAPSPERHPRVQLQKDVRPAYVPAQNLFRDRSGEEPEEMRDC
                                                                                                                                                                                                                                                                                                                              FDMGADLHWQPSRRALEAAYGPEDLDEEEEEEDAPAAGY 11769. .13463
                                                                                             /protein_id="AAD20320.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="penton base"
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/codon_start=1
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/codon_start=1
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Whuman adenovirus type 17.

Whuman adenovirus type 17.

With a Shan viruses, no RNA stage; Adenoviridae; Mastadenovirus.

Chillon, M., Bosch, A., Zabner, J., Law, L., Armentano, D., Welsh, M.J.

and Davidson, B.L.
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ALVDSDAEBSEDEHRPAPFYIPPSGTPGHVAYTYKPITFLDAEGGDMCLHTVEKVDPL
VDNDRYPSHVASFVLAWTRAFVSEWSEFLYEEDRGTPLQDRPIKSVYGDTDSLFVTER
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YALQSLLCPACGRSSKGKLRAKGHAAEALNYELMVNCYLADAQGEDRAKFSTSRMSLK
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LAPGAPATQRWPLYRQPPPHFLVGYQYLVRTCNDYYPDSRAFSRLRYSEVVQPGLQTV
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RMEDSASASDDIERLMHDYYRNLSRCGGQAWGMAERLRIQQAGPKDLVLATIRRLKN
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VSALSLPNGDPPHYREMTGGVFTLRPRERGRAVTETMRRRGEMIERFYDRLPYRRR
RRAPPPPPPEEEIEEVWEEEEEDBAPGDFERFEVRATIAELIRLEDELTVSARNAG
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EEEIEGFMSEIAYQDNSGDVQFILRQPAVNDAEIDSVELSFRFKYTGPYVFTGRRGDLG
DVNRRVYAHASALRAQHRDLPERHADVPLPPLPAGFEPPLPFGARPFFT
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/organism="Human adenovirus type 17"
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complement(4991. .8266)
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Armentano, D. PhD and Souza, D.W.
Direct Submission
Submitted (20-000-1998) Molecular Biology, Ge
New York Ave., Framinham, MA 01701-9322, USA
                                     1871 AGGGCCCATTTCTGCTGGCAGAAGTACGACAAGGTACG 1908
                                                                                                                                                                                                           AF108105 35100 bp DNA VI
Muman adenovirus type 17 complete genome.
AF108105.1 GI:4416335
241 cgcacctggttttgcttcaggaaatatgactacgtccg 278
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complete genome; core protein; DNA polymerase; DNA-binding protein; condprotease; fiber protein; hexon protein; large T-antigen; maturation protein; minor core protein; penton protein; peripentonal hexon-associated protein; promoter; repeat region; peripentonal hexon-associated protein; promoter; repeat region; Human adenovirus type 12. Human adenovirus type 13. Human adenovirus type 13. Human adenovirus type 14. Human adenovirus type 15. Human adenovirus type 15. Human adenovirus type 16. Human adenovirus type 17. Human adenovirus type 18. Human adenovirus type 19. Human adenovirus 
/translation="MPLPCIPPPPVSRDTAACIAWLGLAHASCVDTLRFIKHHDLKIT
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complement(1993. .2343)
                                                                                                                        /codon_start=1
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OSGSIMIEEFHDNAFALLLFIEIRAVALLEAVVEHLENKLQFDLAVIFHQHSGGDRCH
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Submitted (21-7010-1993) J. Sprengel, Institute of Genetics/Dept.
Virology, Weyertal 121, 50931 Cologne 41, FRG
3 (bases 1 to 34125)
2 cck, C., Iselt, A and Doerfler, W.
A unique mitigator sequence determines the species specificity of
the major late promoter in adenovirus type 12 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1806 GCTTTTTGACGGAACGCCAACGTGCAAAAAAAAAGACGAGGTGCGATAACCAGTGGT 1747
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0; Mismatches 167;
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nilarity 47.8%;
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tlanvsevrgipscvgftvloewpipwdmiltdyemfilkrymsvcmccatinvevto
llagherwlihchcorpgslocmsagmilgrwfkmavygalinkrcfwyrevvnhilmp
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VERSION X51800 GI:58543

VERSION X51800.1 GI:58543

KETWORDS GALLY FEGION E4.

SOURCE Human adenovirus type 12.

YILUBES; dSDNA VIRUSES, no RNA Stage; Adenoviridae; Mastadenovirus.

REPERENCE I (Dases; 1 o 3498)

AUTHORS HOGENKAMP, T. and Esche, H.

TITLE Nucleotide sequence of the right 10% of adenovirus type 12 DNA

TITLE encoding the entire region E4

JOURNAL Nucleic Acids Res 18 (10), 3065-3066 (1990)
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Submitted (06-FEB-1990) Hogenkamp T., Institute of Molecular
Blology (cancer Research), University of Essex, Hufelandstr f
4300 Essen 1, F R G
See 
CO0043> for Overlapping sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                1 atggttcttccagctcttcccgctcctcccgtgtgtgactcgcagaacgaatgtgtaggt
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                             others
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                                                                                                                                   Score 54; DB 16;
Pred. No. 3.4e-06;
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                             7250 t
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complement(816..1691)
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Hogenkamp, T.
                                                                                                                                      Query Match 15.7%;
Best Local Similarity 52.2%;
Matches 145; Conservative
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/db_xref-"SWISS-PROT: P03259"
/db_xref-"SWISS-PROT: P03259"
YDLDVESAGEDINEQAVNEFFPESLILAASEGLE-EDEPVILSPVCEPIGGECMPQLHP
EDMDLLCTEMGFPCSDSEDEQDENGMAHVSASAAAAADREREEFGLDHPELPGHNCK
SCEHHRNGTGNTDLMCSLCYLRAYNMFIYSKCAMGGGR"
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WSEKSHLSWDYMLDYMSMQLWRAWLKRRVCIYSLARPLIMPPLPTLQEEKBEERNPAV
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RLTVNLMSRPRLETVYWQELQDEFQRGDMHLQYKYSFEQLKTHWLEPWEDMECAIKAF
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/citation=[6]
/citation=[7]
/citation=[12]
/replace=""
/replace=
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/function="Ela promoter region (-499 to +100)"
369
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1542. 2033
/note="crossref SWISS-PROT:EIBS_ADEL2, P04492"
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/note="crossref SWISS-PROT:ElBL_ADE12, P04491"
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/note="crossref Ad12 EPD07152"
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Shinagawa, M. and Padmanabhan, R.
Comparative sequence analysis of the inverted terminal repetitions from different adenoviruses
Proc. Natl. Acad. Sci. U.S.A. 77 (7), 3831-3835 (1980)
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Spiler,J.A. and van Bree,M.P.
The nuclocitde sequence of the gene encoding protein IVa2 in human
adenovirus type 7
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Juttermann, R., Weyer, U. and Doerfler, W.
Defect of adenovirus type 12 replication in hamster cells: absence of transcription of viral virus-associated and L1 RNAs
J. Virol. 63 (8), 3535-3540 (1989)
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Shibata, L., Zheng, J. H., Koikeda, S., Masamune, Y. and Nakanishi, Y.
Cis- and trans-acting factors for transcription of the adenovirus
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Tolun, A., Alestrom, P. and Pettersson, U.
Sequence of inverted terminal repetitions from different
adenoviruses: demonstration of conserved sequences and homology
Cell 17 (3), 705-713 (1979)
                                                                                                                                                                                                                                                  early region 2b of
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                                                                                                                                                                                                                                                                                                                                                                                     5 (bases 1 to 3957)
van Ormondt, H. and Galibert, F.
Nucleotide sequences of adenovirus DNAs
CLUT: Top. Microbiol. Immunol. 110, 73-142 (1984)
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89150250
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                                                                                                                    (Sires)
(Dases 4831 to 10470)
Shu,L.M., Hong,J.S., Wel,Y.F. and Engler,J.A.
Nucleotide sequence of the genes encoded in human adenovirus type 12
             67 (2), 682-693 (1993)
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Gene 46 (2-3), 187-195 (1986)
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Kimura, T.
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Cell 20 (3), 777
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MCALCYMRLTGHCIFSPISDASGSESSGSPEDTDFPHPLTATPPHGIVRTIPCRVSCR
RRPAVECIEDLLEEDPTDEPLNLSLKRPKCS"
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Pleniazek,N.J., Slemenda,S.B., Pieniazek,D. and Luftig,R.B.
NA RNA region of human enteric adenovirus type 40 shows homology to
the VA region of simian adenovirus type 7
                                                                                                                                                                                                                                                                                                                                                                                                                Vos,H.L., van der Lee,F.M., Reemst,A.M., van Loon,A.E, and Sussenbach,J.S.
France encoding the DNA binding protein and the 23K protease of adenovirus types 40 and 41
Virology 163, 1-10 (1988)
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Bylond, E. A., Telford, E. A., Watson, M. S., McBride, K. and Mautner, V. The DNA sequence of adenovirus type 40

J. Mol., Biol. 234 (4), 1308-1316 (1993)
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The adenovirus type 40 hexon: sequence, predicted structure and relationship to other adenovirus hexons
J. Gen. Virol. 70, 3203-3214 (1989)
                                               Structure and organization of the left-terminal DNA regions of fastidious adenovirus types 40 and 41 Gene 58, 109-126 (1987) 88084437
                                                                                                                                                                                                  Analysis of structure and function of human adenovirus type 40 leftmost 1.85 kb region including transforming ElA gene sapporo Igaku Zasshi 57, 59-66 (1988)
          van Loon, A. E., Ligtenberg, M., Reemst, A. M., Sussenbach, J.S. and Rozijn, T.H.
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Kidd,A.H. and Erasmus,M.J.
Sequence characterization of the adenovirus 40 fiber gene
Virology 172, 134-144 (1989)
89370295
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Human adenovirus type 40.

Human adenovirus type 40.

Yiruses; daDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

1 (sites)

Ishino,M., Sawada,Y., Yaegashi,T., Demura,M. and Fujinaga,K.

Nucleotide sequence of the adenovirus type 40 inverted terminal repeat: Close relation to that of adenovirus type 5

Virology 156, 414-416 (1987)
                      ITFINYEAGDKEKGIMEBANTCLVIHGVYFINESNICVESWNKVSARGCTFYGCWKG
LVGRPKSKLSVKKCLFEKCYLALIYBGDAHIRHNAASENAGFYLLKGMAILKHNMYCG
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QCRFSHSNIMLEPEYFSRVCLMGYFDLSVELCKVIRKNDDTRHRCRQCECGSSHLELR
PIVLNVTEELRSDHLILSCLRTDXESSDEDDN"
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Pred. No. 8.1e-06;
0; Mismatches 167; Indels 0;
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3374. .3808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADRGENOME 34214 bp DNA VR
Human adenovirus type 40, complete genome.
L19443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32306 GCGCGACAGACGGTATCGCT 32287
                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 acgaccaacacgatctcggt 320
                                                                                                                                                  2071. .2073
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                                                                                                                                                                                                                                                                                               2479. .2741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.3%;
Best Local Similarity 47.8%;
Matches 153; Conservative 0
                                                                                                                                                                                                                                                                        /replace-"ga"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L19443.1 GI:303969
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AUTHORS TITLE

REFERENCE

RESULT

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                                                                    VVGRNKSQMSVKKCVFERCIMAMVVEGQARITHNAGSDNVCFLLLKGTASVKHMMICG
GGHSQLLTCADGNCQALRVFHVVSHPRRPWPVFEHNMLMRCTVHLGARRGMFSPYQSN
                                                                                                            FCHTKVLMETDAFSRVWWNGVFDLTMELFKVVRYDESKVRCRPCECGANHIRLYPATL
                                                     VIFMNVRFVVEGFNGTVFASTTQLTLHGVFFQNCSGICVDSWGRVSARGCIFVACWKG
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Vapanstilitatigssvdtaaaaaasaaastargmaadfelxnolaasrlreedals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 33037 AIGCCICTICCGICTCCCTCCACTCCAGIGAGICAAGGCCTITGIAITICI 32978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32857 GCCCTGAAAACTGAAAGAGCGCGACAACGAAACCGTCGATTTGCGAACATTGTTGGCAG 32798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32917 GICAGCAIAICICCACGGGCIGAGGAGCIGITAAGTGGACTGCAGGAGTGGCTGAACGII 32858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tggctgggtgtggcttattctgcggtggtggtgttatcagggcagcggcgcatgaagga 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 aactactacacagagogatctaagoggcgagaccgggggacgcagatctgtttgtcacgcc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 cgcacctggttttgcttcaggaaatatgactacgtccgggcgttccatttggcatgacact 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 atggttcttccagctcttcccgctcctcccgtgtgtgactcgcagaacgaatgtgtaggt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.7%; Score 36.8; DB 16; Length 3 larity 44.7%; Pred. No. 0.79; Conservative 0; Mismatches 177; Indels
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                                                                                                                                  NVTEQLRTDHQMMSCLRTDYESSDED"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                'number-
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Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATA_signal
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HS109F14
LOCUS
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                                                                                                                                                                                                                                                                                                                                      exon
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/translation-"MRMLPDFFTGNWDDMFQGLLETEYVFDFPEPSEASEEMSLHDLF
DVEVDGFEEDANQEAVDGPISDAEGESESGSPEDTDFPHPLTATPPHGIVRTIPCRVS
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                                                                                                                                                                                                                                                                                                                                                                                                        SPEDIDEPHPLIATPPHGIVRIIPCRVSCRRRPAVECIEDLLEEDPIDEPLNLSLKRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product-"ElB"
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                                                                                                                                                                                                                         'number-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'number=2
                                                                                                  /number-
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exon

exon

exon

mRNA

exon

mRNA

exon

CDS

exon

CDS

DEFINITION

SOURCE ORGANISM

ACCESSION VERSION KEYWORDS

REFERENCE
ATHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
REFERENCE
TITLE
JOURNAL

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9350. :22465
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20358. .20498,20576. .20728,20907. .21020)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="dil09F14.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence-not_experimental
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/product-"dJ109F14.1.2 (Transcriptional Enhancer Factor
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join(9350.17140.11789.18692.18753,19629.19763,
17493.17630,17740.17789,18692.18753,19629.19763,
19972.20145,20358.20498,20576.20728,20907.22465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-match: proteins 080701 p28347 p30051 p48984 015561 Q62296 CE02703 p30052; the start codon used for the protein entries is not present in our sequence; we find an ata codon for isoleucine; the ORF continues upstream of this codon, into the next upstream exon where the true start could be located.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                repeat_region
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2. (bases 1 to 170245)

New Philips, S.

Submitted (05-Aug-1998) E-mail enquiries: humquery@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

On Aug 1, 1998 this sequence version replaced gi:3355439.

During sequence assembly data is comparated from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submitssion

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence has been fittle insert of clone 109F14. The true left

end of clone 32948 (287822) is at 13206 in this sequence map criteria

as follows. An attempt is made to resolve all sequencing problems,

such as compressions and repeats, but not necessarily within known

annotated human repeat sequence elements (e.g. Alu). Where the

feature key.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Teature key.

This sequence was generated from part of bacterial clone contigs of This sequence was generated from part of bacterial older the Sanger human chromosome 6, constructed in collaboration by the Sanger content chromosome 6 mapping group and loannis Ragoussis. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6/109F14 is from the library RPCII constructed at the Roswell Park Gancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECIOR: pCYPAC2.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Exparycle; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Exputeria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 170245)
1. (bases 1 to 170245)
1. Tripodish N. Mason, R., Humphray, S.J., Davies, A.F., Herberg, J.A.,
Tripodish N. Mazetic, D., Senger, G. and Ragoussis, J.
Physical map of human 6p21.2-6p21.3: region flanking the
"Genome Res. 8 (6), 631-643 (1998)
98311675
    Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPLIOA gene, a porarrive ZNFIZI LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three polymorphism, complete sequence.
                                                                                                                                                                                                                                                                                                                                                         AL022721.1 GI:3367610
HTG; 60S Hibosomal Protein RPL10A; ca repeat polymorphism; CpG
island; NUCI; NUCI; Nuclear Hormone Receptor 1; Peroxisome
Proliferator Activated Receptor Delta; PPAR-Beta;
PPARB; PPARD; TEF-5; Transcriptional Enhancer Factor; 2NF127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSg repeat: matches 299. .127 of consensus" complement(8496. .8790)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /730. .2875
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complement(6170. .6295)
/note="Alusx repeat: matches 136. .5 of consensus"
6696. .6893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6696 .6893 /note-"MIR repeat: matches 33 .231 of consensus" (872 .6903 /note-"MIRz repeat: matches 88 .119 of consensus" /note-"Alusg repeat: matches 1 .300 of consensus" complement(8324 .8495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .170245
/organ.lam="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="p21.2-21.3"
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/clone_lib="RPCI-1"
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FEATURES

repeat; glial fibrillary acidic repetitive sequence; tandem repeat.

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join(297. .712,1563. .1623,1805. .1900,2833. .2994,3780. .3905; 3414. .4334,5408. .5451,7821. .7906,8551. .8595)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AELRELRILRIDOLTANSARIEVVERDNFAODIGTIRORIODETNIRLEAENNIAAYROE
AHEATLARVDLERKVESLEEEIGFIRKIYEEEVRDLREQLAQOOVHVENDYARDITA
ALREIRTOYEAVATSNMQETEEWYRSKFADITDAASRNAELIROAKHEANDYRROLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MPPRRWSGASGPSRQLGTMPRFSLSRMTPPLPARVDFSLAGALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agfketraseraemmelndrfasyiekvrfleqonkalaaelnqlrakeptkladvyq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTCDLESIRGTNESLEROMREQEERHARESASYQEALARLEEEGGSLKEEWARHLOEY
HDLINVKLALDIELATYRKLLEGEENRITIPVQTFSNLOIRETSLDTKSVSEGHLKRN
    MMGFAPD 9971 bp DNA, ROD 10-FEB-1999 MOUSE gene for glial fibrillary acidic protein (GFAP).
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 9971)

Balcarek, J.M. and Cowan, N.J.

Structure of the mouse glial fibrillary acidic protein gene: implications for the evolution of the intermediate filament multigene family

Nucleic Acids Res. 13 (15), 5527-5543 (1985)
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/note="dinucleotide repeats (TG)6 (TC)9 (AC)8"
/scne="GFAP"
/note="Alu sequence"
/note="2994
/gene="GFAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"glial fibrillary acidic protein"
|protein_id-"CAA26571.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="MGD:MGI:95697"
/db_xref="SWISS-PROT:P03995"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVKTVEMRDGEVIKDSKQEHKDVVM
                                                                                                                                                                                                                                                                                                                                                                                                               1. .9971
/organism="Mus musculus"
                                                                                                    Alu repetitive sequence; direct protein; intermediate filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217. .219
/notem_put. TATA-box"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163. .164
/note="put. CAAT-box"
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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/gene="GFAP"
/note="intron II"
1805. .1900
/gene="GFAP"
/note="exon 3"
/gene="GFAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="intron III"
2377. .2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="cap site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"intron I'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="exon 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197. .8595
/gene="GFAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      713. .1562
/gene="GFAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .563. .1623
'gene="GFAP"
                                                                                                                                                                    Mus musculus
                                                                                                                                                    house mouse.
                                                                               X02801.1
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                                    DEFINITION
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                                                                                                                                               SOURCE
                                                                                                                                                                        IASSRLRLLEYSAFMEVQRDPDTYSKHLFVHIGQTNPAFSDPPLEAVDVRQIYDKFPE
KKGGLKELYEKGPPNAFFLVKFWADLNSTIQEGPGAFYGVSSQYSSADSMTISYSTKV
CSFCKQVVEKVETEYARLENGRFVYRIHRSPMCEYMINFIHKLKHLPEKYMMNSVLEN
                                                                                                        ALAIYPPCGRRKIILSDEGKMYGRNELIARYIKLTGKTRTRKOVSSHIQVLARKKYR
EYQVGIKAMNLDQVSKDKALQSMASMSSAQIVSASVLQNKFSPPSPLPQAVFSTSSRF
                                                                                        translation="ASNSWNASSSPGEAREDGPEGLDKGLDNDAEGVWSPDIEQSFQE"
                                                                                                                                                    WSSPPLLGQQPGPSQDIKPFAQPAYPIQPPLPSTLSSYEPLAPLPSAAASVPVWQDRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Alux repeat: matches 2. .294 of consensus"
24773. .24922
/note="AluSp repeat: matches 127. .297 of consensus"
complement(join(25280. .25484,25713. .25885,26535. .26683,
27037. .27117,21191. .27265,27625. .27644))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
product-"dJ109F14.1.1 (Transcriptional Enhancer Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: cDNas U12404 U12403 X93352 223090; match:
ESTs AA134024 AA148100 AA531410 AA070054 F17880 AA641205
AA745013 AA644024 AA720704 AA888465 AA657588 AA146904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 115386 crcracgaaaaarrraaaaarragccggrergcregcargrecregragrecaggrac 115445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="FLAM" repeat: matches 2. .127 of consensus" 1687* 17186
/note="AluSg repeat: matches 1. .300 of consensus" complement (17298. .17368)
/note="MIR repeat: matches 128. .46 of consensus" 17910. .18225
/note="AluJo repeat: matches 1. .301 of consensus" 18945. .19239
/note="AluSp repeat: matches 2. .298 of consensus" 22414. .22439
/note="13 consensus" 22927. .23234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 cagggcagcggcatgaaggagtttacatagaaccggaagccagggggggcgctggatgc 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                               complement(12114. 12232)
/note="WIR repeat: matches 211. .90 of consensus"
complement(13299. 13434)
/note="AluJo repeat: matches 136. .1 of consensus"
13801. 14075
                                                                                                                                                                                                                                                                                                                                                                                                                                              .296 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MIR repeat: matches 28. .261 of consensus" 5438. .15559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36.2; DB 10; Length 170245; Pred. No. 1.4; 0; Mismatches 68; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Alusx repeat: matches 22.
4303. .14508
                                                                                                                                                                                                                                                                                                      "note="predicted CpG island"
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/db_xref="GI:4490420"
                                                                                                                                                                                                                                                                                   'gene="dJ109F14.1"
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Best Local Similarity 53.1%;
Matches 77; Conservative
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1 3 3 3 3 4 3

/note="exon 4?" 2995. .3779 /gene="GFAP"

intron

mRNA

Db 115506 CGAGATTGTGCTACTGCACTACAGC 115530

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RESULT 11 MMGFAPD/c

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Draft entry and computer readable sequence for [1] kindly submitted by C.Stein, 01-JUN-1989.
Location/Qualifiers
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FTTGFKRLYFLPLQIYGYTLLTLAALNCLGLLHVPLGVFFSLLFLAALILTLFLGFLH
YFRPLNCFWARNYEIIQQPMSYDNLTQRLTVEAAQFIQR"
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l (bases 1 to 773)
Yen, P.H., Marsh, B., Allen, E., Tsai, S.P., Ellison, J., Connolly, L.,
Yen, P.H., Marsh, B., Allen, E., Tsai, S.P., Ellison, J., Connolly, L.,
Nelswanger, K. and Shapiro, L.J.
The human X-linked steroid sulfatase gene and a Y-encoded
pseudogene: evidence for an inversion of the Y chromosome during
primate evolution
Cell 55 (6), 1123-1135 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 cccgcacctggttttgcttcaggaaatatgactacgtccggcgttccatttggcatgaca 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     584 CCCIGAACIGCIICAIGAIGAGGAACIACGAGAICAIICAGCAGCCCAIGICCIAIGACA 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMSISB 2401 bp mRNA PRI 13-JAN-1995
Human steroid sulfatase (microsomal), complete cds.
J04964
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Best Local Similarity 58.7%; Pred. No. 1.9;
Matches 61; Conservative 0; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 ctacgaccaacacgatctcggttgtctcggcgcactccgtacag 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       644 ATCICACCCAGAGGCIAACGGIGGAGGCGGCCCAGTICATACAG 687
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89340479
                                                                                                                                                                                                                                                                                                                                                                                  /product-"steroid sulfatase"
/protein_id="AAA60598.1"
/db_xref="GI:338607"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 t
                                                                                                                                                                                                                                                                                                                                                                       /db_xref-"GDB:G00-120-393"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                         /organism-"Homo sapiens"
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/standard_name="STS-X"
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/note="G00-120-393"
266. .689
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="G00-120-393"
180 c 187 g
                                                                                                                                        Location/Qualifiers
1. .773
                                                                                                                                                                                                                                                                                                                                           'codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J04964.1 GI:338564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
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ACCESSION
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SOURCE
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HUMSTSB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMSTSXG1 773 bp DNA PRI 13-JAN-1995
Human chromosome X steroid sulfatase (STS-X) gene, exon 5 and
flanking regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6260. 6943
/note="region with 19 imp. direct repeats (34 bp)"
/907. 88550
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                                                                                                                                                                                                                                                                                                                               79412 7820
452. 7820
452. 7820
796ne-"16RPD VII" "
7761. 5822
7761. 6143
548. 6143
7761-"region with 7 imp. direct repeats (28 bp)"
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Pred. No. 1.3;
0; Mismatches 55; Indels (
                                                                                                                                                                                                               /dote-"intron VI"
1142. .5208
100te-"homopurine sequence (GA)20 (GAA)9"
5217. .5272
/note-"cr_repeats (GT)24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human blood, cultured fibroblasts or tissue DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mote="exon 9"
9925. :9929
/note="put. polyadenylation signal"
1 2427 c 2672 g 2392 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="intro
/note="intro
8184. .821
/note="(ATT)13 sequence"
8551. .>8551
                    /note="intron IV" 3780. .3905
                        /ou. .3905
/gene="GFAP"
/note="exon 5"
3906. 4117
                                                                                                                   note-"intron V"
                                                                                                                                                                    note-"exon 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.6%;
Matches 69; Conservative
                                                                                     906. .4113
'gene="GFAP"
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                                                                                                                                                                                       1335. .5407
/gene="GFAP"
                                                                                                                                                                                                                                                                                                     408. .5451
gene="GFAP"
                                                                                                                                 114. .4334
gene="GFAP"
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steroid sulfatase.
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BASE COUNT ORIGIN

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MRNA

mRNA

1

RESULT 12 HUMSTSXG1 LOCUS DEFINITION

ORGANISM

19.11

ACCESSION VERSION KEYWORDS SEGMENT SOURCE

MRNA

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GISLTMLRDCREGEGSYFTTGFRRLYFLPLOTYGYTLTLAALNCLGLLHYPLGVFFS
LLFLAALITLIFLGFLHYFRPLNCFMARNYEIIQQPMSYDNLTQRLYGAAGFIQRNF
EPFLLYLSYLHYHTALFSSRDFAGKSQHGYYGDAYEEMDNSVGQILHLLDBLRLAND
TLIYFTSDQAAHVEEVSSKGEIHGGSNGIYGGGANNWEGGIRVBGILHRHYRYIQAGG
KIDEPPSNMDIFPLYAKLAGAPLPEDRIIDGRANDTELGGRSQRSHHFLFHYCNAYI
NAYRWHPQNSTSIWKAFFFTPNFNPVGSNGCFATHVCFCFGSYVTHHDPPLLFHYCNAYI
PRERNELLPASEPREYEILKVWQEAADRHTQTLPEVPDQFSWNNFLWRPPULCCFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation-"MPLRKMKIPFLLLFFLWBABSHBASRPNIILVMADDLGIGDPGC
YGNKTIRTPNIDRLASGGVKLTQHLAASPLCTPSRAAFWTGRYPVRSGMASWSRTGVF
LFTASSGGLPTDEITFAKLLKDQGYSTALIGKWHLGMSCHSKTDFCHHPLHGFNYFY
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Homo sapiens Xp22 bins 29-30 BAC GSHB-227L7 (Genome Systems Human
BAC Library) complete sequence.
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1 (bases 1 to 99033)
Muzny, D., Arenson, A.D., Adams, C., Brundage, E., Bunac, C.,
Carvelli, K., Chacko, J., Chen, J., Di, W., Ding, Y., Dugan, S.,
Durbin, J., Forcum, J., Ganesh, R., Garcia, C., Goodman, M.,
Gorrell, J. H., Haywood, M., Hernandez, J., Jackson, L., Jin, S.,
Kampal, R., Karpathy, S., Kowar, C., Leal, B., Li, Y., Lichtarge, O.,
Liu, W., Logan, O., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L.,
Rashid, N. D., Rowland, K., Savage, L., Scherer, S. E., Shen, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 occycacctggttttgcttcaggaaatatgactacgtccggcgttccatttggcatgaca 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="steroid sulfatase precursor (EC 3.1.6.2)"
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Yen,P.H.
Unpublished (1988)
There is a steroid sulfatase (STS) pseudogene on Yq.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                               note="steroid sulfatase signal peptide"
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Best Local Similarity 58.7%; Pred. No. 2.2;
Matches 61; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                          /note="steroid sulfatase mRNA"
221. .286
/gene="STS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="steroid sulfatase"
1881 a 1440 c 1363 g 1835
Chromosome Xp22.32.
                                                                                                                                 /organism="Homo sapiens"
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221. .1972
/gene="STS"
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     AUTHORS
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FEATURES
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AC005704/c
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KEYWORDS
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EFTASSGGLPDEITFRALLKDOGTSTALIGKHIGASCHKTPSCHAASKRTGVF
EFTASSGGLPDEITFRALLKDOGTSTALIGKHIGASCHKTPSCHASKRTGVF
EFTASSGGLPDEITFRALLKDOGTSTALIGKHIGASCHKTPSCHEDLHGFNYFY
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ELFLAALITILFGFLHYFRPLACFMENNYELIGOPMSYDNLTGRLTVBACFTGNNY
TLIFFSODGAHVERSKOPRGYGGHGGSNGIYGGLANNYEGGINVFGLINGPRUJOAG
KIDEPTSNMDIFPTVAKLAGAPLPEDRILIGGROMPLIGGRSOKSCHEELFHYCNAYL
PRAKHHQNNYSTGINKAPFTPRNPVGSNGCFATHVGFCFGSYVTHHDPPLLFDISKD
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I (bases I to 2429)

Yen, P.H., Allen, E., Marsh, B., Mohandas, T., Wang, N., Taggart, R.T. and Shapiro, L.J.

Cloning and expression of steroid sulfatase cDNA and the frequent occurrence of deletions in STS deficiency: implications for X-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 cccgcacctggttttgcttcaggaaatatgactacgtccggcgttccatttggcatgaca 298
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                                                                                                                                                                                    note="steroid sulfatase signal peptide A (alt.)"
                                                                                                                                                                                                                                                         note="steroid sulfatase precursor (EC 3.1.6.2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204. .266
/gene-"grs"
/note-"steroid sulfatase signal peptide (alt.)"
267. .1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMSTS 6520 bp mRNA PRI 13-JAN' Human steroid sulfatase (STS) mRNA, complete cds.
M16505.
M16505.1 GI:338513
Steroid sulfatase.
Human placenta, CDNA to mRNA, clones M13mp18 and M13mp19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="steroid sulfatase A (alt.)" 637 c 586 g 563 t
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10.2%; Score 35.2; DB 9;
Best Local Similarity 58.7%; Pred. No. 2;
Matches 61; Conservative 0; Mismatches 43;
                                                               note="steroid sulfatase mRNA"
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464 bp upstream of KpnI site.
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                                                                                                                                                                                                                                                                                     codon_start-1
                                                                         204. .1955
/gene="STS"
204.
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2 (bases 2430 to 6520)
                                                                                                                                         04. .272
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/gene="STS"
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/gene="STS'
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BASE COUNT ORIGIN

å 셤 à d DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT

REFERENCE AUTHORS TITLE JOURNAL MEDLINE MEFERENCE

0; Gaps

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17654..17684
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27530. .28319
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complement(28320. .28563)
family="LTR8"
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19. 26587
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6494
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/rpt_family='NER'
complement(19909. .20144)
rytt_family='NER20'
complement(20635. .20938)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               omplement(27042. .27156)
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. . . 24839
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pt_family="AluJb"
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t_family="MLT1F"
plement(23968. .24092)
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15815. 15835
/rpt_family="An_rtch"
15849. 16022
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complement(16848. 170
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omplement(25883. .26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pt_family-"LlPA12"
            complement(14285. .14
rpt_family="(GAAA)n"
4493. .14773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family-"L1PA12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family="(CA)n" . .26674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L1PB3"
                                                                                                                                                                                                                                                                                                                                                                   family-"AluJo" . 22072
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   rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                      .21637
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                                                                                           Direct Submission
Submitted (26-SEP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
                                                                                                                                                                                                                                                                                                                                        Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.

Location/Qualifiers
                                                                                                                                                                                                                                                                                Sequence similarities were identified using Powerblast by Jinghui Zhang.
Simon, M., Stovall, K., Timms, K.M., Todd, J., Vo, Q., Williamson, A., Worley, K.C., Yu, W., Chinault, C., Nelson, D. and Gibbs, R.A. Direct Submission
                                                                                                                                                                                                                              The repeat regions shown were identified using RepeatMasker by Adrian Smit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  546. .4841
rpt_family="Alux"
complement(join(4947. .5371,7132. .7254,7357. .7478,
1980-"Human steroid sulfatase (STS)"
note="M16505 incomplete sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cloue_llb="Genome Systems Human Bac Library"
1065. .1348
/rpt_family="MER7B"
1352. .1649
/rpt_family="Alusx"
1673. .1754
/rpt_family="MER7B"
4011. .4317
/rpt_family="Alusx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(12735. .13019)
/rpt_family="AluJo"
complement(13060. .13141)
/rpt_family="LiPB3"
13951. .14026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="MLT1A1"
complement(11568. .11849)
/rpt_family="AluJo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /standard_name="DXS6767"
/db_xref="GDB:345311"
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/db_xref="taxon:9606"
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/map="Xp22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y="(TAGA)n"
f674
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/rpt_family="(TAGA)n"
complement(6535. .6659)
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39. .10140
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67. .6926
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/rpt_family="AluSg"
10550. .10010
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omplement(7521. .77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone-"GSHB-227L7"
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                                                                                      Complement (3332. 33622)
/ Tyte_family="LikB6"
Complement (3332. 33736)
/ Tyte_family="LikB6"
Complement (3374. 33797)
/ Tyte_family="LikB6"
/ Tyte_family="THELC"
Complement (3425. 34493)
/ Tyte_family="THELC"
/ Tyte_family="LikB6"
/ Tyte_family="LikB6"
/ Tyte_family="LikB6"
/ Tyte_family="LikB1"
/ Tyte_family="LikB2"
     complement(32791. .33249) /rpt_family-"MER83"
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10.2%; Score 35.2; DB 11; Length 99033; Pred. No. 2.7; DB 11; Length 99033; Pred. No. 2.7; DB 11; Length 99033; Pred. No. 2.7; DB 11; Length 99033; DB 12; Dcal Similarity SB 7%; Pred. No. 2.7; DB 11; Length 99033; DB 12; Dcal Similarity SB 7%; Pred. No. 2.7; DB 11; Length 99033; DB 12; Dcal Similarity SB 12; Dcal Similarity SB 12; DB 11; Length 99033; DB 12; Dcal Similarity SB 12; DB 11; Length 99033; DB 12; Dcal Similarity SB 12; DB 11; Length 99033; DB 12; Dcal Similarity SB 12; DB 11; Length 99033; DB 11; Length 99033; DB 12; DB 12; DB 11; Length 99033; DB 12; DB 12;

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Search completed: June 23, 2000, 09:36:27 Job time: 12569 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                          OM protein - protein search, using sw model
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Run on:

June 23, 2000, 09:07:32; Search time 20.4 Seconds (without alignments) 341.359 Million cell updates/sec

Title:

US-09-214-478-2 1594 1 MITSGVPFGMILRPIRSRLS.....RALLQHHRPILMHDYDSIPM 294

188963 Perfect score: 1594

Sequence: 1594

I MTTSGVPFGMTLRPTRSRLS....RALLOH

Gapop 10.0, Gapext 0.5

Gapop 10.0, Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Searched: 188963 seqs, 23686106 residues

Manimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	ticoi		RAG1 pro	restric	Open reading frame	2/neu		v	Б	Klebsiella pneumon	Glycerol-3-phospha	lula	Mature durum wheat	Alcohol-oxidase. N	HER4 with alternat	占	HER4. New recombin	or tyr	₩		Rhodopsin. Diagnos	nbinant	Her2-GM-CSF immuno	mutant	mutant	ATM mutant C9140T.	mutant	ATM mutant 7279del	ATM mutant 5435del	ATM mutant 8578del	mutant	nutant	O	Ataxia-telangiecta
SUMMARIES	CI CI	19	2	5	묾	W48269	W01111	W92406	W03549	W57324	W60255	W30680	R08222	W62647	P60229	R54843	R91734	R54841	R91733	W82002	R38483	R93116	R11606	W19764	W19691	W19692	W19690	W19694	W19695	W19697	W19693		96	a	Н
	8	1																															Н		
	Length	534	294	383	191	458	1255	1255	265	391	391	391	624	369	664	1058	1058	1308	1308	271	348	348	664	782	2998	3001	3046	3053	3054	3055	3055	3066	3026	3056	3056
di	Query Match	6	99.3		•	•	4.6	٠	4.6	4.6	4.6	4.6	•	4.5	•	•	4.4		4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4
	Score	1589	1583	101.5	88.5	75.5	~	74	73.5	73	73	73	72	71	7.1	6	ö	70.5	0	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	. 70
		-	7	e	4	ហ	φ.	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	26	27	28	29	30	31	32	33	

Human ataxia telan ATM mutant 5319ins Murine Ataxia-tela Polypeptide encode Canine distemper v Env polypeptide of Fragment H501789 o Interleukin-8 rece Interleukin-8 rece Recombinant high a ATM mutant C1240T.
W84269 W19696 W36178 W06833 W68334 R28033 W56444 R80756 R80756
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ALIGNMENTS

RESULT W03197

ឧទ	W03197 standard; Protein; 534 AA.
2 5	140-1907 (first partry)
1 C	Jucocorticold receptor/adenoviral ORF6 chimaeric fusion protein.
3	Human adenovirus; inverted tandem repeat; E4; E1; open reading frame;
KW	expression; late gene; cell line; defective recombinant adenovirus;
ΚW	complementation; gene therapy; cystic fibrosis; dystrophy; PCR;
ΚW	neurodegenerative disease; blood coagulation disorder; viral infection;
ΚW	primer; amplification; polymerase chain reaction; fusion protein.
os	Homo sapiens/Adenovirus Ad5.
PN	WO9622378-A1.
5	25-JUL-1996.
PF	19-JAN-1996; F00088.
PR	20-JAN-1995; FR-000/4/.
E E	01-JUN-1995; FR-006532.
7 t	OG-SERTING FAR-OLDURAL STATE OF SERVICES O
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4 2	WPT: 96-354535
áĉ	1.1.1. COURT TAIL TO THE TAIL TAIL TO THE TAIL TAIL TAIL TAIL TAIL TAIL TAIL TAIL
Ē	Cells for produ. of recombinant adeno and adeno-associated virus
Ē	contain part of the E4 region of adeno virus, used to produce new
Ľď	adeno virus defective in El and E4 regions for use as gene therapy
PT	vectors
PS	Example 1; Page 41-43; 69pp; French.
႘	The invention relates to novel cell lines which can support the
ខ	replication and production of defective recombinant addnoviruses which,
ខ	lack all or part of the El and E4 regions. The novel cell lines contain
႘	the adenoviral E4 region, esp. the open reading frame 6 and/or /,
ខ	inserted into its gene under control of a promoter, prer . Irom MMIV which
ខ	is regulated by dexamethasone. The E4 ORFb may also be inserted into the
႘	genome as a chimaeric fusion gene comprising a glucocorticold receptor
ខ	hormone binding domain fused N-terminally to the adenoviral Okro gene.
ပ္ပ	The fusion protein generated (this sequence) is retained in the cycopiasm
ပ္ပ	of the cell in the absence of hormone by interaction of the hormone
႘	binding domain with the hsp90 protein or other factors. Contacting the
ខ	fusion protein with the hormone causes translocation of the protein to
ខ	the cell's nucleus were the ORF6 product functions. The gene was
ខ	generated by amplifying the sequence encoding the hormone binding domain
ខ	with primers T31316-7 and recombining the fragment with the adenoviral
ខ	ORF6 sequence. The defective viruses generated in the new Cells Can De
႘	used for gene therapy e.g. for cystic fibrosis, dystrophy,
႘	neurodegenerative diseases, blood coagulation disorders, Viral
ပ္ပ	infections, etc
•	

Gaps Query Match 99.7%; Score 1589; DB 1; Length 534; Best Local Similarity 100.0%; Pred. No. 2.6e-164; Matches 293; Conservative 0; Mismatches 0; Indels (

534 AA;

Seguence

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Page

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PR 04-JUN-1996; U10245.

PR 04-JUN-1995; US-462014.

PR 07-1995; US-462014.

PR 27-OCT-1995; US-549489.

PR 159-043152/04.

PR Recombinant adeno-associated virus contg. second gene which racing a demonstrates its conversion from single stranded to double stranded to virus - enhances efficiency of ex vivo transduction into target cell prample 1; page 72-73; 131pp; English.

PR Recombinant adeno-associated to double stranded to the intervent of the muse mammary tumour virus promoter and the sample 1; page 72-73; 131pp; English.

CT This is the amino acid sequence of the product of the human adenovirus comes placed under control of the mouse mammary tumour virus promoter and a growth hormone terminator sequence and used to create the minigene in comparises at least 2 selected genes; the first gene able to express the comparises at least 2 selected genes, the first gene able to convert the single stranded virus to its double stranded form upon expression.

CT he rAAV is useful in pharmaceutical compositions for use in ex vivo and convert of inverse the prany for the treatment of inherited diseases, cancer and convert the convert of the single stranded for the preparation of interest and convert the single stranded virus for the interpret of interest of the companion of interest of the companion of the convert of the single stranded for the preparation of interest and convert the single stranded virus of the companion of the convert of t
                                                                                                                                                                                                    RGRHLIYLLHYDGHVGSVVPAMSFGYSALHCGILNNIVVLCCSYCADLSEIRVRCCARR 241
                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                  "Human Ad5 E4 region ORF6 encoded by plasmid pMMTVE4ORF6 minigene. "Human Ad5 E4 region ORF6 encoded by plasmid pMMTVE4ORF6 minigene. Minigene; human adenovirus type 5; open reading frame; promoter; in variouse mammary tumour virus; growth hormone; terminator; recombinant; packaging cell line; adeno-associated virus; ex vivo; gene therapy; inherited disease; cancer; genetic dysfunction; cystic fibrosis.

Human adenovirus type 5.
                                      VRGLPCSVGFTLIQEWVVPWDMVLTREELVILRRCMHVCLCCANIDIMTSMMIHGYESWA
                                                                                                                                                              LHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFIWYREVVNYNMPKEVMFMSSVFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genetic dysfunctions, e.g. cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "encoded by codon CAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "encoded by codon TTG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W01729 standard; Protein; 294 AA.
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other genetic dysfunc
Sequence 294 AA;
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Score 1583; DB 1; Length 294;
Pred. No. 5.1e-164;
1; Mismatches 1; Indels (
Query Match
Best Local Similarity 99.3%;
Matches 292; Conservative
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61 YVRGLPCSVGFTLIQEWVVPWDMVLRREELVILRKCMHVCLCCANIDIMTSMMIHGYESW 120 à

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PR Act and human FRAGI nucleic acid and related proteins - used for Rat and human FRAGI nucleic acid and related proteins - used for diagnosis of neoplasis, particularly osteosarcoma Claim 13; Fig 4; 35pp; English.

Claim 13; Fig 4; 35pp; English.

Claim 13; Fig 4; 35pp; English.

Come I (FRAGI) protein of the invention. When expressed in frame with FGFR2 (fibroblast growth factor receptor 2), the FRAGI gene with FGFR2 (fibroblast growth factor receptor 2), the FRAGI gene can be used as a hybridisation probe to detect chromosomal capormalities, particularly a rearrangement that fuses FRAGI to another companies, particularly a rearrangement that fuses FRAGI to another companies is used to diagnose neoplasia, specifically osteosarcoma.

Crearrangements is used to diagnose neoplasia, specifically osteosarcoma.

Crearrangements is used to diagnose neoplasia, specifically of Gentify related genes in other species. Agents that inhibit FRAGI (e.g. antibodies or antisons molecules) may be useful therappeutically and the FRAGI protein can also be used to screen for drugs. Antibodies are used for purification of the FRAGI protein; in cloning FRAGI alleles and the FRAGI protein; in cloning FRAGI alleles and the remains and the fraginal part and as probes in protein blots and the fraginal Rat FRAG1 protein. Fibroblast growth factor receptor activating gene 1; FRAG1; rat; FGFR2; fibroblast growth factor receptor 2; transforming activity; osteosarcoma; autophosphorylation activity; chromosomal abnormality detection; 61 YVRGLPCSVGFTLIQEWVVPWDMVLTREELVILRKCMHVCLCCANIDIMTSMMIYGYESW 120 241 RTRRIMLRAVRIIAEETTAMLYSCRIERRRQQFIRALLQHHRPILMHDYDSTPM 294 18-JUN-1997; U10660. 18-JUN-1997; U2-020009. 18-JUN-1996; US-020009. LOYEN UV, MIKI T; WPI; 98-061151/06. 1. .129 /note= "signal peptide" /note= "encoded by GIG" 245 /note= "encoded by CAC" 130. .383 /note= "mature FRAG1" Location/Qualifiers W41592 standard; Protein; 383 AA. W41592, 18-JUN-1998 (first entry) Misc_difference 185 383 AA; Misc_difference .mmunoassays neoplasia. Rattus sp. Seguence Key Peptide Protein ٣ 121 241 121 RESULT W41592 ò g g à 셤 δ

11 TLRPTRSRLSRRIPYSRDRLP------PFETETRATILEDHPLLPECNTLTM 56 57 HNVSYVRG------LPC---SVGFTLIQEWVVPWDMVLTRE-ELVILRKCM--HV 99 40 SLRPIPERWPRLIPLLLRPAPFHSPPGWAGAPGSAPLATGVRPP--SHHYLGPSAQDPSR 97 89; Query Match 6.4%; Score 101.5; DB 1; Length 383; Best Local Similarity 22.2%; Pred. No. 0.0057; Matches 66; Conservative 36; Mismatches 106; Indels 89;

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Gaps

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us-09-214-478-2.rag

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The present sequence represents RHK1 used from an example of the present invention which describes a Hansenula mrakil protease resistant killer protein. The killer protein has antibacterial activity and so can be used in an antibacterial agent which contains the killer protein as the active component. The killer protein can also be used as the active component in an antibacterial soop. The protein, which was derived from the yeast Hansenula mrakil, has antibacterial properties and may be used in sterilising and cleaning compositions e.g. soap. recombinantly in a large amount.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 MMIHGY-----ESWALHCHCSSPGSLQCIAGGQ-----VLASWFRMVVDGAMFNQRF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 VSYVRGLP-----CSVGF--TLIQEWVVPWDMVLTREELVILRKCMHVCLCCANIDIMTS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 LEVITRYPRILPDLWSSLCH---PLRKNAVLNANPAKTIPFVLIASNFIGVLFSRSLHYQF 374
                                                                                                                                                                                ID NO:6 from J10075789 Example 2. HM-1; RHK1; Hansenula mrakii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 VPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMM---DEEAFNDKRFHLALLISHLIALTT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hansenula mrakii protease resistant killer protein – has antibacterial properties and may be used as active ingredient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualiflers
676. .1255
/label= Intracellular_domain
/note= "claimed domain, useful for immunisation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding HER-2-neu poly:peptide(s) - used for prevention or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HER-2/new protein.
HER-2/new c-erbBi; pl85; oncogene; tyrosine protein kinase;
HER-2/new; c-erbBi; pl85; oncogene; tyrosine grancer;
presst cancer; ovary cancer; colon cancer; lung cancer;
prostate cancer; immunisation; tumour; vaccine; vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.7%; Score 75.5; DB 1; Length 458; 19.5%; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 I-WYREVVNYNMPKEVMFMSSVFMRGRHLIYLRLWYDGH 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | : : : : | : : | CANTAILLIEWSGMPFFVG-----PIWYVLH 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. soap
Example 2; Page 10-12; 16pp; Japanese.
                                                                                                       23-JUN-1998 (first entry)
Open reading frame RHK1 protein SEO
Killer protein; protease resistant;
yeast; mutant; antibacterial; soap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W01111 standard; Protein; 1255 AA
                                                                        Ą.
                                                                        W48269 standard; Protein; 458
                                                                                                                                                                                                                                                                                                                                                             24-MAR-1998.
04-SEP-1996; 234393.
04-SEP-1996; JP-234393.
(EIJI-) EIJIN KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 19.5%
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-CCT-1996.
28-MAR-1996; U01689.
31-MAR-1995; US-414417.
(UNIW ) UNIV WASHINGTON.
Cheever. MA, Disis ML;
WPI; 96-455361/45.
N-PSDB; T40739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 98-244362/22.
N-PSDB; V20655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W01111;
01-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
W01111
RESULT
W48269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   쉱
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 H-CGWRRGGALEPQISFESLPCQSLACGFESDKWYGVP--LILDRDGILVRLRFIWVALI 154
                                                                                                                                                 :|| : |: |: |: || || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.3 || 1.
                                                                                                                                                                                                                                                     153 MFNQRFIWYREVVNYNMPKEVMFMSSVFMRGRHLIYLRLWYDGHVGSVVPAMSFGYSAL- 212
                                                                                                                                                                                                                                                                                                   of EBV - for treating Epstein-Barr virus infection, infectious mononucleosis, Hodgkar's disease, Burkitt's Infection, infectious Disclosure; Page 11-12; 20pp; English.

The oligonucleotides given in 039617-18 are selectively hybridisable to the BHREI gene (039619). The antisense oligonucleotides can be used to treat EBV infection in patients suffering from infectious mononucleosis, Hodgkin's disease, Burkitt's lymphoma, undifferentiated nasopharyngeal carcinoma, AIDS related lymphoma or angioinmunoblastic lymphadenopathy. They can also be used to treat EBV-induced proliferating diseases by treating bone marrow from a patient to destroy proliferating tumour cells, then reimplanting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 QSTPXYVVDLSVRGMLEASEGLDGW-IHQQ-------GG-----WGTLIEDNIPGS 161
                                                                                                           CLCCANID----IMTSMMIHGYESWALHCHCSSPGSLQCIA---GGQVLASWFRMVVDGA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 77; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 TLRPTRSRLSRRTPYSRDRLPPFETETRATILEDHPLLPEC------NTLTMHN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 RINFSLNVVENLALLVLTYVSSSEDFTIHENA------FIVFIAASLSYMLLTC 290
                                                                                                                                                                                                                                                                                                                                                                                                   ----HCGILNNIVVICCSYCADLSEIRVRCCARRTRRLMLRAVRIIAEETTAMLYSC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-00T-1993 (first entry)

BamHI restriction fragment 1 (BHRFI) gene product.

Antisense oligonucleotide; hydridisation; EBV;

Infection; infectious mononucleosis; Hodgkin's disease;

Burkitt's lymphoma; undifferentiated nasopharyngeal carcinoma;

AIDS related lymphoma; angloimmunoblastic lymphadenopathy;

EBV induced proliferative disease; bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New anti-sense oligo-nucleotide which hybridises with BHRFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.6%; Score 88.5; DB 1; 123.3%; Pred, No. 0.058; tive 18; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORFIWYREVVNYNMPKEVMFMSSVFMRGRH 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 RRFSWTLFLAGLTLSLLVICSYLFISRGRH 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R37813 standard; Protein; 191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 23.3%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hickish T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CANC-) CANCER RES INST.
Cunningham D, Hickish 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        marrow into the patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUN-1993.
04-DEC-1992; G02256.
05-DEC-1991; GB-025891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Epstein-Barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 93-197083/24.
N-PSDB; Q39619.
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Gaps

37;

60; Indels

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15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158
                                                                                                                                                                                                                                                                                                                                                                                                    387 SNTAPLOPEQLOVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQ 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447 GLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   585 VACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDD---KG 641
                                                                                                                                                                                                                                                                                                                                                                                                                                               GLPCS------VGFTLIQE------KVVPWDMVLTREELVILR------KCMH 98
                                                                                                                                                                                                                                                                                                                                                                  ---TMHNVSY---VR 63
                            Claim 2: Page 56-61; 71pp; English.

Human HER-2/neu protein (W01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also I40739). The protein is over-expressed in various cancers, including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host calls for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        З
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell; B cell; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 VCLCCANIDIMTSMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       535 LRGOECVEECRVLQGLPRE----YVNARHCLPCHPECQPQNGSVT---CFGPEADQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507 EGLACHOL------CARGHCWGPGPTQCVNCSO-----F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 IWYREVVN----YNMPKEVMFMSSVFMRGRHLIYLRLWYDGHVGSVVPAMSFGYSALHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GILNNIVVLCCSYCADLSEIRVRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                To Use of HER-2/neu polypeptides - for eliciting an immune response an HER-2/neu associated malignancy, particularly for treating or
                                                                                                                                                                                                                                                                                      4.6%; Score 74; DB 1; Length 1255;
18.2%; Pred. No. 28; 'tive 34; Mismatches 117; Indels 136;
treatment of malignancies with which the HER-2/neu oncogene is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  676. 1255
/note= "region which elicits immune response"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 CARRTR-----RIMLRAVRIIAEETTAMLYSCRIERRRQQF----IRALLQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | : | | : : | | | 642 CPAEQRASPLTSIISALIGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQ 692
                                                                                                                                                                                                                                                                                                                                                                20 SRRTPYSRDRLPPFETETRAT ---- ILEDHPLLPECNTL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W92406 standard; Protein; 1255 AA.
W92406;
21-APR-1999 (first entry)
HER-2/neu oncogene protein.
HER-2/neu; oncogene; immune response;
malignancy; treatment; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 18.29
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR : 01-APR-1996; 625101.
PR : 01-APR-1996; US-625101.
PR : 17-MAR-1999; US-03364.
PR : 31-MAR-1995; US-414417.
PR : 31-MAR-1995; US-414417.
PR : 31-MAR-1995; US-414417.
PR : 91-1993; US-414417.
PR : 91-1993; US-414417.
PR : 91-15235/13.
PR : 91-15235/13.
                                                                                                                                                                                                                                1255 AA;
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                      associated
                                                                                                                                                                                                                                  Sequence
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Region
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W92406
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ORF-5 protein sequence from BamHI fragment of HVT.
Herpes virus of turkey; open reading frame; ORF; homology; vector;
avian herpes virus; recombinant viral vaccine; intergent region; IBDV;
cytomegalovirus immediate early promoter; UL55 gene; repeat region; ILTV;
antigen; infectious bursal disease virus; Marek's disease virus; MDV;
infectious laryngotracheitis virus; avian aneamia virus; vaccination;
infectious bronchitis virus; IBV; poultry; Gumboro disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N. PSDB: T39209.

N. PSDB: T39209.

Live recombinant avian vaccine - comprises herpes virus as vector and having sequence encoding antigenic polypeptide inserted between UL55 gene and repeat region

Example 4: Fig 1; 50pp; French.

This is the amino acid sequence of the protein encoded by the open reading frame 5 (ORF-5) from the Bamil I fragment from the herpes virus of turkeys (HVT). The DNA fragment was isolated from HVT strain FC126 (J. Gen. Virol.). 70:1799-1804 (1989)) and is used as a basis for generating live recombinant viral vaccines using the herpes virus DNA sequences as vectors. The fragment contains 3 intergenic regions into which genes encoding heterologous proteins to be expressed can be linserted, preferably under control of the cytomegalovirus immediate early (CWV-IE) promoter. The heterologous proteins can be used to vaccinate
response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence. Sequence 1255 AA;
                                                                                                                                                                                                                                                                                           | ::| |:| ::| || 387 SNTAPLQPEQLQVFETLEEITGYLYISAWÞDSLPDLSVFQNLQVIRGRILHNGAYSLTLQ 446
                                                                                                                                                                                                                                                                                                                                                                                       447 GLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                         99 VCLCCANIDIMISMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRWVVDGAMFNQRF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     535 IRGOECVEECRVLOGLPRE-----YVNARHCLPCHPECQPQNGSVT---CFGPEADQC 584
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                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                ----TMHNVSY---VR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             585 VACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDD---KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IWYREVVN----YNMPKEVMFMSSVFMRGRHLIYLRLWYDGHVGSVVPAMSFGYSALHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 507 EGLACHQL------CARGHCWGPGPTQCVNCSQ-----F
                                                                                                                                                                           CARRTR-----RIMLRAVRIIAEETTAMLYSCRTERRRQQF----IRALLQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                642 CPAEQRASPLISIISAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQ 692
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30-DEC-1994; FR-016017.
(INMR) RHONE MERIEUX SA.
Audonnet JCF, Bublot MJM, D
Laplace ELF, Riviere MAE;
WPI; 96-364150/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Newcastle disease.
Herpesvirus of turkey
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Matches
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us-09-214-478-2.rag

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poultry against Gumboro disease (caused by IBDV), Newcastle disease,
Marek's disease, infectious bronchitis, infectious laryngotracheitis and
avian anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PT Former young.

Fermentative production of glycerol using recombinant host -

Fortaining genes for glycerol.3-phosphate dehydrogenase and-or

FJ glycerol.3- phosphatase

FJ glycerol.3-phosphatase

Claim 9; Page 31-32; S7pp; English.

CC This Saccharomyces polypeptide comprises a cytosolic

GL glycerol.3-phosphate dehydrogenase (G3DBH) that catalyses the

CC conversion of dlydroxyacetone phosphate to glycerol.3-phosphate.

CC Glycerol.3-phosphatese (G3DBH) that catalyses the

CC Groversion of dlydroxyacetone phosphate to glycerol.3-phosphate.

CC Groversion of dlydroxyacetone phosphatese (G3PBH) see also

CC Groversion of dlydroxyacetone phosphatese (G3PBH) see also

CC Groversion of glycerol.3-phosphatase (G3PBH) see also

CC The glycerol obtained is used in cosmetics, liquid soaps,

CC The glycerol obtained is used in cosmetics, liquid soaps,

CC The glycerol obtained is used in cosmetics, liquid soaps,

CC The glycerol obtained is used and antifreezes; its esters are used in commenced to the oil and fat industries. The method produces glycerol rapidly some.
                                                                                                                                                                                                                                                                                                                                                                                 89 ELVILRK--CMHVCLCCANIDIMTSMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFR 146
                                                                                                                                                                                                                                                                                                                                                                                                                                      173 QLMDSRKILCLYESAMÇDN -----PGAQGMILSCYCGRPGGLQCLAFIRTLEMLFN 223
                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 HQFLPRICSQLKGHVDSHVRAISCLKGFEVGAKGVQLLSSYIT-EELGI-----QCGAL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W57324 standard; Protein; 391 AA.
W57324;
14-SEP-1998 (first entry)
Cytosolic glycerol-3-phosphate dehydrogenase GPDI.
Glycerol-3-phosphate dehydrogenase; G3PDH; GPDI; DARI; OSGI;
D2830; YDL022W; yeast.
                                                                                                                                                                                                                                 Query Match
4.6%; Score 73.5; DB 1; Length 265;
Best Local Similarity 29.4%; Pred. No. 3.8;
Matches 20; Conservative 9; Mismatches 28; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE W57324 standard; Protein; 391 AA.

AC W57324

DE Cytosolic glycerol-3-phosphate dehydrogenase GPD1.

E Cytosolic glycerol-3-phosphate dehydrogenase; G3PDH; GPD1; DARI; OSG

Saccharomyces sp.

COS Saccharomyces sp.

E Cytosolic glycerol-3-phosphate dehydrogenase; G3PDH; GPD1; DARI; OSG

Saccharomyces sp.

E Cytosolic glycerol-3-phosphate dehydrogenase; G3PDH; GPD1; DARI; OSG

Saccharomyces sp.

E Cytosolic glycerol-3-phosphate SL, Hsu AK, Lareau RD; DR NW191998-297943762.

E C Containing genes for glycerol-3-phosphate dehydrogenase and glycerol-3-phosphates glycerol-3-phosphate dehydrogenase (G3PDH) that catalyses containing genes for glycerol-3-phosphates (G3PDH) that catalyses conversion of dlydroyenase (G3PDH) transformed with a conversion of monor, oligo, polysecolificm a variety of the oliming either a G3PDH gene and/or a G3P gene and then of the presence of a monor, oligo, polysecolificm and fat industries. The method produces glycerolifically without generation of polluting by-produces and inaxpensively without generation of polluting by-produces and inaxpensively and the presence of and enaxpensively and the presence of and enaxpensively and and enachped by-produces and enaxpensively and and enachped by-produces and enaxpense glycerolificm and enachped by-produces recombined by-produces and enaxpense glycerolificm and 
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4.6%; Score 73; DB 1; Length 391;
Best Local Similarity 23.2%; Pred. No. 7.4;
Matches 45; Conservative 21; Mismatches 58; Indels
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                                                                                                                            Seguence
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W57324
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New method for increasing production of 1,3-propane:diol - comprises

Termentation of inexpensive carbon sources by microorganism
expressing dehydratase, used, e.g. to prolong half-life of enzyme
bisclosure; Page 65-66; 133pp; English.

The sequence is that of cytosolic glycerol-3-phosphate dehydrogenase;
The sequence is that of cytosolic glycerol is maproved by
this sexting a method of fermentative production
the transformant in presence of a carbon source (e.g. mono-, oligo-
to poly-saccharide or I substrate) convertible to 1,3-pd;
The transformant in presence of a carbon source (e.g. mono-, oligo-
typelic compounds: 1,3-pd can now be produced by a single
recombinant organism from inexpensive carbon sources such
a glucose (rather than costly glycerol or dihydroxyacetone),
caping and without causing pollution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPLLPE-CNTLIMHNVSYVRGLPCSVGFTLIQEWVVPWDMVLTREELVILRKCMHVCLCC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 ANIDIMTSMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFIWYRE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 VVNYNMPKEVMFMSSVFMRGR-----HLIYLRLWYDG--HVGSVVPAMSFGYSALHCGIL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70; Gaps
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23.2%; Pred. No. 7.4;
Live 21; Mismatches 58; Indels
                                                                                                                                                                                 Klebsiella pneumoniae glycerol-3-phosphate dehydrogenase. glycerol-3-phosphate dehydrogenase; production; 1,3-propanediol; recombinant. Klebsiella pneumoniae. W09821341-A2.
                                                                                                                                                                                                                                                                                                13-NOV-1997; U20873.
113-NOV-1996; US-030601.
(GENY ) GENENCOR INT INC.
Chase MW, Diaz-torres M, Dunn-coleman NS, Trimbur
WPI; 98-297944/26.
                                                                                                                            W60255 standard; Protein; 391 AA.
W60255;
28-SEP-1998 (first entry)
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W30680;
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                                 245 KNVVALGCGFVEGL 258
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217 NNIVVLCCSYCADL
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Best Local Similarity
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12-001-1998 (first entry) Glycerol-3-phosphate dehydrogenase GPD1. Glycerol-3-phosphate dehydrogenase; GPD1; 1,3-propanediol.

Saccharomyces sp. W09821339-A1. 22-MAY-1998.

2001 ± 40 te 40 - 1 1 1 1 1 1 2 1 1 1 - 1 1 1 1 2 2 1 1 1 - 1 1 1 2 2 1 1 1

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W62647 standard; Protein; 369 AA.
W62647;
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      PF 10-NOV-1997; U20292.

PA (UDUPO ) DU POWER DENGUES.

PA (CERW ) GENENCOR INT INC.

PA (CERW ) GENENCOR INT INC.

PI 13-NOV-1996; U3 CASCADOROUS & CO E I.

PA (CERW ) GENENCOR INT INC.

PI NAGAREN OF GENENCOR INC.

PI NAGAREN OF GENENCOR INC.

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PI NAGAREN OF MAIL RW, Nakamura CE, Payne MS, Picataggio SK,

PI NAGAREN OF MAIL RW, Nakamura CE, Payne MS, Picataggio SK,

PI NAGAREN OF MAIL RW, Nakamura CE, Payne MS, Picataggio SK,

PR CASCADA OF MAIL RW, Nakamura CE, Payne MS, Picataggio SK,

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PR CASCADA OF MAIL RW, Nakamura CE, Payne MS, Picatagraphic of using PR CASCADA.

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CC CASCADA OF MAIL RW, Nakamura CE, 13-Propanediol CI, Comprises

CC CASCADA OF MAIL RW, Nakamura CE, 13-Propanediol CI, Comprises

CC CASCADA OF MAIL RANGE CONTROLES.

CC CAS
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Extracellular portion of the human epidermal growth factor receptor 2.
Human epidermal growth factor receptor 2; HER2; waccine; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 VVNYNMPKEVMFWSSVFMRGR-----HLIYLLMYDG--HVGSVVPAMSFGYSALHCGIL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1997; UZ0292.

13-NOV-1996; US-030601.

(DUPO) DU PONT DE NEMOURS & CO E I.

(GEMV ) GENENCOR INT INC.

Dias-Torres M, Gatenby AA, Haynie SL, Hsu AK, Lareau RD,

Dias-Torres W, Nakamura CE, Payne MS, Ploataggio SK,

Trimbur DE, Whited GM;

WPI: 98-297942/26.
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/4. .84
/label= epitope
//note= "potential T-cell epitope"
/13. .130
/label= epitope
//note= "potential T-cell epitope"
/note= "potential T-cell epitope"
/note= "potential T-cell epitope"
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(GETH ) GENEATECH INC.

Hudziak RM, Shepard HM, ullrich A;
HWF1: 90-735946/50.

N-PSDB: Q06828.

The least 9 amino acid(s) prepd. using expression vector of DNA to least 9 amino acid(s) prepd. using expression vector of DNA isolated from human epidermal growth factor receptor

Disclosure; Fig 13: 49pp; English.

This claimed sequence is free of transmembrane or intracellular portions of the HERZ mol. The protein is antigenic in animals.

Fragment comprising at least 9 amino acids open several possibilities for further research and a broad range

C foptential therapeutic apllications, e.g. for the treatment of mammanary gland adenocarcinoma and other cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ::| ||| | ::| ||| 366 SNTAPLQPEQLQVFETLEEITGYLYISAWRDSLPDLSVFQNLQVIRGRILHNGAYSLTLQ 425
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4.5%; Score 72; DB 1; Length 624;
Best Local Similarity 19.7%; Pred. No. 18;
Matches 52; Conservative 24; Mismatches 92; Indels 96; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 GLPCS------VGFTLLQE-----WVVPWDMVLTREELVILR-----KCMH 98
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/label- epitope
/note- "potential T-cell epitope"
433. .443
/label- epitope
/note- "potential T-cell epitope"
519. .529
/label- epitope
/note- "potential T-cell epitope"
/note- "potential T-cell epitope"
305. .315
/label= epitope
/note= "potential T-cell epitope"
327. .353
/label= epitope
/note= "potential T-cell epitope"
375. .385
/label= epitope
/note= "potential T-cell epitope"
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18-MAY-1990; U02697.
19-MAY-1989; US-354319.
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12;

Mon Jun 26 09:10:34 2000

New DNA sequences coding for oxido:reductase(s) and other enzyme(s) - useful for expression in microorganisms to give high yields for bleaches and detergents.

Disclosure: Fig 11A-11B: 99pp; English.

The gene encoding this protein (EC-1.1.3.13) is used (in combination with its regulatory sequences and/or those of dihydroxyacetone-synthetase) to produce genetically engineered microorganisms that produce oxidases or other enzymes in yields that allow industrial application on a large scale. The engineered yeasts can produce oxidases having improved properties with respect to their application in oxidation reactions and/or in bleaching and (UNIL) UNILEVER NV. Ledeboer AM, Verrips CT, Visser CT, Janowicz ZA, Hollenberg WPP: 86-063249/10. N-PSDB: N60174. P60229 standard; Protein; 664 AA. 01-AUG-1991 (first entry) 25-JUL-1985; 201235. 27-JUL-1984; EP-201114. 07-FEB-1985; GB-003160.

352 LITNGIEAGVKIRPTEEELATADEDFRRGYAEYFENKPDKPLMHYSVISGFFGDHTKIPN 411 467 126 : : : : | | : : 1 | . : 468 ARRMESFAGEVISHPLFKVDSPARARDLDLETCSAYAGPKHLTANLYHG--SWTVPIDK 525 89 The DNA encoding this sequence is identical with that of HER4 (Q64896) up to nucleotide 3168, where the sequence diverges and the ONF stops after 13 amino acids, followed by an extended, unique 3'-UTR.
HER4 is the fourth member of the EGFR-family of tyrosine kinases and is expressed in some human cancers and in some tissues of neuronal or muscle origin. HER4 polynucleotides, opt. labelled, are useful in assays (e.g. of HER4 mRNA to detect certain neoplasms, esp. Sequence 1058 AA; HER4 with alternate 3'-end without AP domain. Human epidermal growth factor receptor; HER; EGF; tyrosine Kinase; cancer; neuronal tissue; muscle tissue; neoplasm; 412 GKFMTMFHFLEY----PFSRGFVRITSANPYDAPDFDPGFLNDERDLWPMVWAYKKSRET New recombinant nucleic acid expressing HER4 - a new receptor tyrosine kinase expressed in some cancer cells, and related vectors, antibodies, ligands etc, for diagnosis and treatment of DB 1; Length 1058; carcinoma; primer; probe; PCR; autophosphorylation domain; 4.4%; Score 70.5; D 24.5%; Pred. No. 53; :1ve 20; Mismatches CNTLIM-HNVSYVRGLPCSVGFTLIQE-----EP-599274-A.
01-JUN-1994.
23-NOV-1992; 118837.
24-NOV-1992; US-981165.
CHRIM) BRISTOL-MYERS SQUIBB CO.
CLIOUSCOU J. Plowman GD, Shoyab M; WPI; 94-169599/21. Location/Qualiflers 34. .3210 R54843 standard; Protein; 1058 AA. R54843; cancers Claim 12; Fig. 2A; 104pp; English. (first entry) Query Match
Best Local Similarity 24...
Best Local Similarity 24...
Conservative 34. .3210 /*taq= a 127 SSPGSLOCIAGGOV 140 PTPKNDFHVTSNQV N-PSDB; Q64898 Homo sapiens 11-JAN-1995 526 NESS OF THE PROPERTY OF THE PR à à g ò

40;

Length 369;

Search completed: June 23, 2000, 10:03:34 Job time: 3362 sec

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Indels

73;

DB 1; Length 664;

1 MITSGVPFGMILRPIRSRLSRR-IPYSRDRLPPFEIETRAILE-------DHPLLPE 50 .: | | : : | | : : | : : | : : | : : |

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121 ALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMF-NQRFIWYREVVNYNM 169

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Gaps

46; Indels 17;

us-09-214-478-2.rai

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June 23, 2000, 09:17:15 ; Search time 45.41 Seconds (without alignments) 93.473 Million cell updates/sec
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Sequence 68, Appl
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Sequence 68, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 60, Appl
Sequence 50, Appl
Sequence 60, Appl
Sequence 61, Appl
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1594
1 MITSGVPFGMILRPIRSRLS......RALLQHHRPILMHDYDSTFM 294
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-467-083-68
US-08-414-4178-68
US-08-418-4178-68
US-08-65-5458-68
US-08-65-5101-2
US-08-951-300-2
US-08-991-300-2
US-08-991-300-2
US-08-991-300-2
US-08-98-5
US-08-484-438-4
US-08-484-438-2
US-08-484-438-2
US-08-482-108-1
US-09-146-283-4
US-08-85-5665-50
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US-08-55-2408-50
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    protein search, using sw model

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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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	#1.22	1; 66; C:
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	9-28 8, Applicatic 157028191 NT SP028191 NT SP028191 NT Red, JG NT SATO, TE NT NEWTION: OF SEQUENCES: ONDENCE ADDRE SSEE: Campbe 1: A370 La J San Diego 1: California San Diego 1: California RX: USA 92122 R READABLE FO M TYPE: Flop TYPE: Flop TYPE: Flop TYPE: Campbe 17. AGE TING SYSTEM: ARE: DATE ARE: DATE ARE: DATE APPLICATION NUMBER	11aı Cor SRLS
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еееееееееееееееееееееееееееееееееееее	SSULT  Sequence 28, Applicatic Sequence 28, Applicatic Sequence 28, Applicatic GENERAL INFORMATION: APPLICANT: Reed, Jo APPLICANT: Seto, TaTILE OF INVENTION: UTILE OF INVENTION: UNMBER OF SEQUENCES: CORRESPONDENCE ADDRESSEE: Campbe STREET: A370 La J CITY: San Diego STATE: California CONTRY: USA ZIP: 92122 COMPUTER READABLE FO MEDIUM TYPE: Flop APPLICATION NUMBER FILING DATE: CLASSIFICATION NUMBER FILING DATE: CLASSIFICATION NUMBER FILING DATE: TELEPHONE: (619) 53: INFORMATION FOR SEQ ID SEQUENCE CHARACTERIS! TELEPHONE: (619) 53: INFORMATION FOR SEQ ID SEQUENCE CHARACTERIS! TOPPLOGY: linear	try Mit Los ches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 VS------YVRGLPCSVGFTLIQEWVVPWDMYLTREELVILRKCMHVC--LCCA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 TLHPVLELAARETPL---RLSPEDT----VVLRYHVLLEEIIERNSETFTETWNRFITHT 76
                        -----NTLTMHN 58
59 VS------YVRGLPCSVGFTLIQEWVVPWDMYLTREELVILRKCMHVC--LCCA 104
                                                                                                          -----GG-----WSTLIEDNIPGS 161
                                                                        105 N-----IDIMTSMMI---HGYESWALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.6%; Score 88.5; DB 4; Length 191; Best Local Similarity 23.3%; Pred. No. 0.013; Matches 49; Conservative 18; Mismatches 66; Indels 7
                                                                                                                                                                                                                                                                                                      APPLICANT: LA JOLIA CANCER RESEARCH FOUNDATION
TITLE OF INVENTION: Interaction of Proteins Involved in
TITLE OF INVENTION: a Cell Death Pathway
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 TLRPTRSRLSRRTPYSRDRLPPFETETRATILEDHPLLPEC--
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119 QSTPYYVVDLSVRGMLEASEGLDGW-IHQQ-----
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                                                                                                                                                                                162 RRFSWILFLAGLTLSLLVICSYLFISRGRH 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION NUMBER: 37,643
REFERENCE/DOCKET NUMBER: FP-LJ 1361
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                             RESULT 2
PCT-10595-04600-28
Scquence 28, Application PC/TUS9504600
GENERAL INFORMATION:
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: USA
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162 RRFSWILFLAGLTLSLLVICSYLFISRGRH 191

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APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: TO DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHIC
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHIC
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 68
ADDRESSEE: Seed and Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 IWYREVVN----YNMPKEVMFWSSVFMRGRHLIYLRLWYDGHVGSVVPAMSFGYSALHC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        585 VACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDD---KG 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447 GLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVG 506
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Best Local Similarity 18.5%; Pred. No. 0.42;
Matches 65; Conservative 34; Mismatches 116; Indels 136; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               507 EGLACHOL------CARCHCWGPGPTQCVNCSQ------F
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                                                                                                                                                                                                                           ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 SRRTPYSRDRLPPFETETRAT ---ILEDHPLLPECNTL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,083
FILLING DATE: 06-JUN-1995
CLASCYFOLCATION: 424
              Sequence 68, Application US/08467083 Patent No. 5726023 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 372836 SEBDANBERRY
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
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TOPOLOGY:
US-08-467-083-68
US-08-467-083-68
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                               CITY: Seattle
STATE: Washing
US-08-486-348A-68
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                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214
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                                                                                                     APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: TO DIAGNOSIS AND TREATHENT OF MALIGNANCIES IN WHICH THE TITLE OF INVENTION: FOR DIAGNOSIS AND TREATHENT OF MALIGNANCIES IN WHICH THE TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry LLP
STREET: 6500 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
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18.5%; Pred. No. 0.42;
tive 34; Mismatches 116; Indels 136; Gaps
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                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,417B
FILING DATE: 31-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     920010.448C2
                                                  Sequence 68, Application US/08414417B Patent No. 5801005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
CLASSIFICATION: 424
ATTONNEY AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 9200
REFERENCE/DOCKET NUMBER: 9200
TRIBECOMMUNICATION: (200).622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 18.5%
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: amino acid; TOPOLOGY: linear US-08-414-4178-68
                                                                                                                                                                                                                                                                                                                                                      98104-7092
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APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387 SNTAPLOPEOLOVEETLEETICYLYISAWPDSLPDLSVFONLOVIRGRILHNGAYSLTLQ 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GILNNIVVLCCSYGADLSEIRVRC 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.4%; Score 86; DB 2; Length 1255;
Best Local Similarity 18.5%; Pred. No. 0.42;
Matches 65; Conservative 34; Mismatches 116; Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 CARRTR-----RLMLRAVRIIAEETTAMLYSCRTERRRQGF----IRALLQ 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOOTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY APACTATION: 424
                                                                                                                                                                                                                                                                                               E: Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
Sequence 68, Application US/08486348A Patent No. 5846538 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFRENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                         Washington
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US-08-468-545B-68

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15;
                         APPLICANT: Cheever, Martin A.

PEPLICANT: Dista, Mary L.

TILLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TILLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TILLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
TILLE OF INVENTION: ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 VCLCCANIDIMTSMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 IWYREVVN-----YNMPKEVMFMSSVFMRGRHLIYLRLWYDGHVGSVVPAMSFGYSALHC 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.6%; Score 74; DB 2; Length 1255;
Best Local Similarity 18.2%; Pred. No. 11;
Matches 64; Conservative 34; Mismatches 117; Indels 136; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 SRRIPYSRDRLPPFETETRAT----ILEDHPLLPECNTL-----TMHNVSY---VR 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPEN Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,101
FILING DATE: 01-APR-1996
                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G:
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION:
TELEPHONE: (206) 632-6931
INFORMATION: C26) 632-631
INFORMATION FOR SEQ ID NO: 2:
SEGUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-625-101-2
                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
7TP: 98104-7092
   SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214
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                                                                                            APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columna Center, 701 Fifth Avenue
CITT: Seattle
STATE: Washington
COUNTRY: 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       447 GLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVG 506
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18.5%; Pred. No. 0.42;
tive 34; Mismatches 116; Indels 136; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 SRRIPYSRDRLPPFETETRAT----ILEDHPLLPECNTL------TMHNVSY---VR 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Was:

COUNTRY: US

ZIP: 98104-7092

ZIP: 98104-7092

COMPUTER READBLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,545B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SABATERY, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 32,629
REFERENCE/
Sequence 68, Application US/08468545B Patent No. 5876712 GENERAL INFORMATION:
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; Sequence 2, Application US/08356786 ; Patent No. 5877305

US-08-356-786-2

RESULT 7 US-08-625-101-2 ; Sequence 2, Application US/08625101 ; Patent No. 5869445

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Sequence 11, Application US/08968563
Patent No. 6013494
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US-08-968-563-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-968-563-11
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4.6%; Score 74; DB 2; Length 1255;
Best Local Similarity 18.2%; Pred. No. 11;
Matches 64; Conservative 34; Mismatches 117; Indels 136;
                                                 APPLICANT: Houston, L. L.
TAPPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer TITLE OF INVENTION: MARKER
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmind R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 CARRTR-----RIMLRAVRIIAEETTAMLYSCRTERRRQQF----IRALLQ 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION 424

RECOR PAPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27/829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
          Huston, James S.
Oppermann, Hermann
                                                                                                                                                                                                                                                  CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-356-786-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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104 ANIDIMISMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFIWYRE 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: NEW YORK
COUNTRY: U.S.A.
COMPUTER READALE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
APPLICATION NUMBER: US/08/968,563
                                                                                                                                                                                                                                                                                                                                                               5: E. I. DU PONT DE NEMOURS AND COMPANY 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.

21P: 19898
ADDRESSEE: GENENCOR INTERNATIONAL, INC.
STREET: 4 CAMBRIDGE PLACE
STREET: 1870 SOUTH WINTON ROAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,601
FILING DATE: NOVEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETRY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9982
TELECHOME: 302-812
TELEPHOME: 302-773-0164
                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHOD FOR THE TITLE OF INVENTION: PRODUCTION OF 1 NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOU
                                                                                                                                                                        VASANTHA NAGARAJAN
MARK S. PAYNE
STEPHEN K. PICATAGGIO
RAMESCH V. NAIR
CHARLES E. NAKAMURA
ANTHONY A. GATENBY
AMY (KUANG-HUA) HSU
RICHARD D. LA REAU
                                                                                                             MARIA DIAZ-TORRES
DONALD E. TRIMBUR
GREGORY M. WHITED
                                                                                            HARON L. HAYNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: GPD1
                                                                                                                                                                                                                                                                                                                                                                                                       WILMINGTON
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                                                                               RESULT 11
5240838-5
;Patent No. 5240838
                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQ ID NO:5:
; LENGTH: 664
5240838-5
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US-08-484-438-4
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                                               1164 NYNINAPKEVMFMSSVFMRGR----HLIYLRLWYDG--HVGSVVPAMSFGYSALHCGIL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 ------ECNTLTMHNVSYVRGL-----PCSVGFTLIQEWVVPWDM--VLTREELVI 92
                                                              DDS. 197 TVAXHIPKD-----FRGEGKDVDHKVLKALFHRPYFHV-SVIEDVA-GISI--CGAL 244
        --ET 196
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MERCHITELLI, CINZIA
APPLICANT: MERCHITELLI, CINZIA
APPLICANT: CARDELLI, CINZIA
APPLICANT: CARDELLI, LOTSA ERCOLI
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF A GENE
TITLE OF INVENTION: ENCODING A LOW MOLECULAR WEIGHT GLUTENIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.5%; Score 71; DB 2; Length 369;
illarity 21.3%; Pred. No. 4;
Conservative 18; Mismatches 49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPHICATION NUMBER: US/08/991,300
FILING DATE: 16-DEC-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT MI 96/A 002663
FILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F:
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2264-0201-0X
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                RESULT 10
US-08-991-300-2
; Sequence 2, Application US/08991300
; Sequence 2, Application US/08991300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                        APPLICANT: D'OVIDIO, RENATO APPLICANT: PORCEDDU, ENRICO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703-413-3000
DD. 180 SGANIATEV---AQEHWS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRKCMHVC--LCCANI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: prote#n
US-08-991-300-2
                                                                                                                                 217 NNIVVLCCSYCADL 230
                                                                                                                                                                          Db 245 KNVVALGCGFVEGL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 29; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
ZIP: 2220
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RESULT 11
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69 VGFTLIQEWVVPWDMVLTREELVILRKCMH-----VCLCCANIDIMTSMMIHGYESW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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4.4%; Score 70.5; DB 2; Length 1058;
Best Local Similarity 24.5%; Pred. No. 21;
Matches 27; Conservative 20; Mismatches 46; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ALHCHCSSPGSLQCIAGGOVLASWFRMVVDGAMF-NQRFIWYREVVNYNM 169
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"APPLICANT: Plowman, Gregory D.
"APPLICANT: Culousou, Jean-Michel
APPLICANT: Culousou, Jean-Michel
APPLICANT: Siegall, Clay B.
APPLICANT: Helistr m, Ingegerd
APPLICANT: Helistr m, Ingegerd
APPLICANT: Helistr m, Ingegerd
APPLICANT: Helistr m, Karl E.
TILLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
KOMRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,438
FILING DATE: 07-JUN-1995
                                                                                                       FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

**APPLICATION NUMBER: 08/323,442

FILING DATE: 14-OCT-1994

**APPLICATION NUMBER: 08/150,704

FILING DATE: 10-NOV-1993

CLASSIFICATION DATA:

**APPLICATION NUMBER: US 07/981,165

FILING DATE: 24-NOV-1992

CLASSIFICATION: 530

ATTORNEY, AGENT INFORMATION:

NAME: MASCOCK, S. Leglie

REGISTRATION NUMBER: 5624-230

**APPLICATION NUMBER: 5624-230

TELECOMMUNICATION INFORMATION:

**INFORMATION FOR SEQ ID NO: 4:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
от-дек: US/08/484,438
07-JUN-1995
N: 530
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元章atent, No. 5811098
577Patent No. 5811098 5780031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-438-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
GY: linear
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69 VGFTLIQEWVVPWDMVLTREELVILRKCMH-----VCLCCANIDIMTSMMIHGYESW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Sealfon, Stuart C.
TITLE OF INVENTION: Cloning and Expression of
TITLE OF INVENTION: Cloning and Expression of
TITLE OF INVENTION: Gonadotropin-Releasing Hormone Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ATREET: 1155 Avenue of the Americas
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-ZIJ1
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PCOS/MS-DOS
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: 17-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Lealie
REGISTRATION UNBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 1308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ALHCHCSSPGSLQCIAGGOVLASWFRMVVDGAMF-NQRFIWYREVVNYNM 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.4%; Score 70.5; DB 2; Best Local Similarity 24.5%; Pred. No. 29; Matches 27; Conservative 20; Mismatches 46;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: 0S 08/150,704
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leelie
REGISTRATION NUMBER: 5524-230
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08390000A Patent No. 5985583
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ELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-484-438-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-08-390-000A-8
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Search completed: June 23, 2000, 10:04:33 Job time: 2838 sec
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                                                                                                                                                                                                                                                       81 WDMVLTREELVILRKCMHVCLCCANIDIMTSMMIHGYE-SWALHCHCSSPGSLQCIAGGQ 139
                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                               140 VLASWFRMVVDG------AMFNQRFIWYREVVNYNMPKEVMF 175
                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 348;
                                                                                                                                                                                                                    37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Hudzlak, Robert M.

APPLICANT: Shepard, H. Michael

APPLICANT: Ulrich, Axel

TITLE OF INVENTION: HER2 EXTRACELLULAR DOMAIN

NUMBER OF SEQUENCES: 2

ADDRESSE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTAL

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING NATA:
                                                                                                                                                                             Query Match 4.4%; Score 70; DB 2
Best Local Similarity 20.9%; Pred. No. 4.8;
Matches 23; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIEICATION: 435

"PRIOR APPLICATION DATA:
"APPLICATION UNMER: 08/355460

PRIOR APPLICATION UNMER: 08/048346

APPLICATION NUMBER: 08/048346

FILING DATE: 15-APR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/354319

FILING DATE: 19-MAY-1989

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08422108
Patent No. 6015567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lee, Wendy E. REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 554
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 415/225-1994
                                           348 amino acids
amino acid
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acid
                                                                                              , MOLECULE TYPE: protein US-08-390-000A-8
                                                                                  TOPOLOGY:
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20 SRRIPYSRDRLPPFETETRAT----ILEDHPLLPECNTL------TMHNVSY---VR 63
                                                                                                              426 GLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVG 485
                                                                                                                                                                                                                                                99 VCLCCANIDIMISMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRWVVDGAMFNQRF 158
                                                                                                                                                                                                                                                                                            -----F 513
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                                                                                                                                                                                                                                                                                                                                                              64 GLPCS-----VGFTLIQE----WVVPWDMVLTREELVILR------KCMH 98
                                       Gaps
                                       :96
Length 624;
                                       92; Indels
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4.4%; Score, 70; DB 3;
19.7%; Pred. No. 11;
tive 24; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                         214 GILNNIVVLCCSYCADLSEIRVRC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VACAHYKDPPFCVARC 579
  Query Match
Best Local Similarity 19.7%
Matches 52; Conservative
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM protein - protein search, using sw model	June 23, 2000, 09:36:35 ; Search time 61.02 Seconds (without alignments) 282.484 Million cell updates/sec	US-09-214-478-2 1594 1 MITSGVPFGMILRPIRSRLSRALLQHHRPILMHDYDSIPM 294	BLOSUM62 Gapop 10.0 , Gapext 0.5
	OM protein - pro	Run on:	Title: Perfect score: Sequence:	Scoring table:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	E4 34K	E4 34K	E4 17K	E4 33K	protein	hypothetical prote	ਰ	hypothetical prote	rhodopsin - Africa	hypothetical prote	hypothetical prote	opsin, rod - Pomat		E2 protein - human	NADH dehydrogenase	hypothetical prote	probable respirato	pectate lyase (EC	NADH dehydrogenase	opsin, ultraviolet		$\sim$	G,				hypothetical prote	$\boldsymbol{\omega}$	thetica	н
	DI	Q4ADC2	S10867		Q4 ADM1		_	A			: T16796															T244	S454	T322	S652	T231	A406
	Length DB	294 1							1603 2																						
& Ouerv	!	100.0	53.9	20.8	11.7	5.6	ა ა	5.4	5.1	5.1	5.0	•	5.0			4.9		4.9	4.8	4.8			4.8	4.8		4.7	4.7	4.7	4.7	4.7	4.6
	Score		828.5	331	186.5	88.5	87	85.5	82		79.5	•		79	78	•	77.5	77.5	77	77	76.5	76.5	76.5	92	92		75.5	74.5	74.5	74.5	74
Result	Š.		~	m	4	ហ	ဖ	7	۵	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23		ż	56	27	,		

protein-tyrosine k NADH dehydrogenase NADH dehydrogenase probable iron-aulf protein kinase A-r protein kinase A-r hypothetical prote glycerol-3-phospha glucosylceramidase complement C5a ana	NADH dehydrogenase NADH dehydrogenase NADH dehydrogenase ABC transporter sl phospholipase C ho
A24571 T14056 125797 C64757 S00726 TVHUAE T25821 S40059 S27357	S41829 T11059 T11149 S77032 T42440
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1255 346 4446 604 604 391 3515	459 459 459 790 1898
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ALIGNMENTS

168808

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR 63:*
1: pir1:*
2: pir2:*
3: pir3:*

Database :

168808 segs, 58629743 residues

Searched:

\	RESULT	1	*
\	04ADC2		Marie Care
	early E4	E4 34K protein - human adenovirus 2	2.5
	C; Spec		
	A; Note		•
	C; Date	C.Date: 02-Apr.1982 #sequence_revision 02-Apr.1982 #text_change 04-Mar-1994	• .
	C; Acce	400000000000000000000000000000000000000	
	R; Heri	R; Herisse, J.; Rigolet, M.; Dupont de Dinechin, S.; Galibert, F.	
	Nuclei	eic Acids Res. 9, 4023-4042, 1981	the carboard torth
	A; Titi	A)TILLE: Nucleotide sequence of adenovitus 2 Dns itayment encourns for A:Reference number: A93733: MIID:82059444	See Consens out
	A: Acce	A; Accession: A03805	
	A; Mole	A; Molecule type: DNA	1. J.
	A; Resi	A;Residues: 1-294 <her></her>	The second secon
	A; Note	A; Note: this probable protein was assigned by correlating EM data and Sl	argestro
	C; Gene	C, Genetics:	X XI
	A; Map	A; Map position: 92.0-93.4 C.C.monfemili: adonovirus pariv RA 34K nrotoin	
	C; Key	i	
			*** *** *** ***
	Quer Best	100.0%; Score 1594; DB 1; Length 294; nilarity 100.0%; Pred. No. 9.3e-142;	
	Matc	Matches 294; Conservative 0; Mismatches 0; Indels 0; G	Gaps U;
	οy	1 MITSGVPFGMILRPIRSRLSRRIPYSRDRLPPFETETRATILEDHPLLPECNILIMHNVS	9
	QQ	1 MTTSGVPFGMTLRPTRSRLSRRTPYSRDRLPPFETETRATILEDHPLLPECNTLTMHNVS	09
	οy	61 YVRGLPCSVGFTLIQEWTVPWDMYLTREELVILRKCMHYCLCCANIDIMTSMMIHGYESW	120
	q	61 YVRGLPCSVGFTLIQEWVVPWDMYLTREELVILRKCMHVCLCCANIDIMTSMMIHGYESW	120
	δý	121 ALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFIWYREVVNYNMPREVMFMSSVF	180
	qq	121 ALHCHCSSPGSLQCIAGGQVLASWFRWVVDGAMFUQRFIWYREVVNYNMPKEVMFMSSVF	180
	å	181 MBCBHLIXIBIMYDGHVGSVVPBMSFGYSALHCGILNNIVVLCCSYCADLSEIRVRCCAR	240
	ÿ		
	qq	181 MRGRHLIYLRLWYDGHVGSVVPAMSFGYSALHCGILNNIVVLCCSYCADLSEIRVRCCAR	240
	Qy	241 RTRRIMLRAVRITAEETTAMLYSCRTERRRQOFIRALLQHHRPILMHDYDSTPM 294	•
	Dp	241 RIRKIMLRAVRIIAEETTAMLYSCRIERRRQOFIRALLQHHRPILMHDYDSIPM 294	•

RESULT S10867

_______ B4K protein - human adenovirus 12 C;Species: Mastadenovirus h12 (human adenovirus 12) C;Decis 20-Feb-1995; #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999 C;Accession: S10867; S3952 R;HogenKamp, T.; Esche, H.

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of two isolates of mouse a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: C93065; A03743
R; Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A; Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi A; Reference number: A93065; MUID: 85035713
A; Accession: C93065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BHRF1 protein - human herpesvirus 4 (strain B95-8)
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 23-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1992 #sequence_revision 30-Jun-1992 #text_change 04-Mar-1994
                                                                                      61 YVRGLPCSVGFTLIQEWVVPWDMYLTREELVILRKCMHYCLCCANIDIMTSMMIHGYESW 120
                                                                                                                                                                                               121 ALHCHCSSPGSLQCIAGGQVLASW------FRMVVDGAMFNQRFIWYREVVNY 167
                                                                                                                                                                                                                                                 67 -----SPPVEQPQVGQQPVAQQLDSDMNLSELPGEFINITDERLARQETVWNITPKNM 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 CMHVCLCCANIDIMTSM--MIHGYESWALHCHCSSPGS-----LQCIAGGQVLASWFR 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 MYYDGAMFNQRFIWYREVYNYNMPKEYMFMSSVFMRGRHLIYLRLWYDGHVGSVVPAM-- 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 SFGYSALHC-GILNNIVVLCCSYCA-DLSEIRVRCCARRTRRLMLRAVRIIAEETTAM-- 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 RIGGGVIFCESLISCYVVIVCQCCACPPIDAQVDHCMRLLSFTLRRWQNLLLGRSGSSPL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 NPLTMS--ATLSRMDCCVGLPHCMGWLPSPVGAVAFVMEGALPIPWSYYLNSYDKHVLQQ 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 NILIMHNVSYVRGLPCSVGFTLIQEWV------VPWDMVLTREELVILRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Ball, A.O.; Beard, C.W.; Villegas, P.; Spindler, K.R. Virology 180, 257-265, 1991
A;Title: Barly region 4 sequence and biological comparison A;Title: Barly region 4 Sequence and biological comparison A;A;Reference number: A38519; WUID:91082417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 186.5; DB 1;
; Pred. No. 4.7e-10;
43; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Mastadenovirus musl (mouse adenovirus 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E4 34K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 IPGFDIPRNRTERLRQRMLHRFYSYRTPIYRLTY
                                                                                                                                                                                                                                                                                                                                       168 NMPKEVMFMSSVFMRGRHLIYLRLWYDG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: host Mus musculus (house mouse)
C; Date: 30-Jun-1992 #sequence revieton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.7%;
24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-288 <BAL>
A;Cross-references: GB-N37187
C;Superfamily: adenovirus early
C;Reywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.7%
Best Local Similarity 24.8%
Matches 68; Conservative
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C; Date: 02-Apr.1982 #sequence_revision 02-Apr.1982 #text_change 12-Apr.1996
C; Date: 02-Apr.1982 #sequence_revision 02-Apr.1982 #text_change 12-Apr.1996
C; Date: 03-Apr.1982 #sequence_revision 02-Apr.1982 #text_change 12-Apr.1996
C; Date: 03-Apr.1982 #sequence_revision 02-Apr.1982
R; Herisse, J.; Rigolet, M. Dupont de Dinechin, S.; Galibert, F.
A; Ridolet Acids Res. 9, 4023-4042, 1981
A; Reference number: A93733; MUID:8205944
A; Reference number: A93733; MUID:8205944
A; Recession: A03804
A; Recession: A03804
A; Residues: 1-153 «HER>
A; Note: these probable proteins and the introns in the coding regions were assigned by c; Genetics:
C; Genetics:
A; Map position: 91.8-95.2
A; Introns: 61/3
C; Superfamily: adenovirus early E4 17K protein
F; S6-153/Product: early Protein
F; S6-153/Product: early E4 10K protein #status predicted <TPP>
                                    ent
'Nucleic Acids Res. 18, 3065-3066, 1990
-Ancleic Nucleic Sequence of the right 10% of adenovirus type 12 DNA encoding the A. Reference number: $10860; MUID:90272430
-A. Recession: $10867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Species: Mastadenovirus h2 (human adenovirus 2)
Note: host Homo sapiens (man)
Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 12-Apr-1996
Accession: A03804
                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:X73487; NID:g313361; PIDN:CAA51901.1; PID:g313386 Superfamily: adenovirus early E4 34K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PWDMVLTREELVILRKCMHVCLCCANIDIMTSMMIHGYESWALHCHCSSPGSLQCIAGGQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 VLASWFRMVVDGAMFNQRFIWYREVVNYNMPKEVMFMSSVFMRGRHLIYLRLWYDGHVGS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVPAMSFGYSALHCGILNNIVVLCCSYCADLSEIRVRCCARRTRRIMLRAVRIIAEETTA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 RRIPYSRDRLPPFETERAII-LEDHPLLPECNTLIMHNVSYVRGLPCSVGFTLIQEWVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 53.9%; Score 858.5; DB 2; Best Local Similarity 55.0%; Pred. No. 6.2e-73; Matches 149; Conservative 52; Mismatches 69;
                                                                                                                                                                                                                R;Sprengel, J. submitted to the EMBL Data Library, June 1993 Reference number: S33928 A;Accession: S33952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             early E4 17K protein 1 - human adenovirus 2 N; Contains: early E4 10K protein
                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA A; Residues: 1-227, 'CA', 230-291 <SPR>
                                                                                                                                  A;Molecule_type: DNA
A;Residues: 1-291 <HOG>
A;Cross_references: EMBL:X51800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match

Best Local Similarity 38.5v

Matches 80; Conservative
                                                                                                         Status: preliminary
                                                                                                                                                                                                                                                                                                                         Status: preliminary
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õ 셤 A; Molecule type: DNA A; Residues: 1-191 <BAN>

1 I MITSGVPFGMILRPIRSRISRRIPYSRDRLPPFETETRATILEDHPLLPECNTLIMHNVS 60

76;

42; Indels

Length 153;

20.8%; Score 331; DB 1; 38.5%; Pred. No. 7.2e-24; 10; Mismatches

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formate dehydrogenase (EC 1.2.1.2) gamma chain - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A70390
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:AE000720; NID:92983529; PIDN:AAC07109.1; PID:92983534; GB:AE00
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Map position: 4
A;Introns: 18/1; 57/3; 75/2; 120/1; 168/2; 194/1; 258/1; 302/2; 348/3; 392/3; 442/1;
                                                                                                                                                                                                             Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666
A;Accession: A70390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL:277134; PIDN:CAB00874.1; GSPDB:GN00022; CESP:R09H10.5
ce: clone R09H10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein R09H10.5 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999 C; Accession: T24098 R; Basham, V. Submitted to the EMBL Data Library, July 1996 A; Reference number: 219840 A; Accession: T24098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 GMTLRPIRSRLSRRIPYSRDRLPPFETETRATILEDHPLLPECNTLTMHNVSVV----R 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 WVVFLSAIVFFLTGILMMFPENFSMGLVRWSVVIHEITFIIAGAFTIIHIYMATVGVPGS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --CSSPGS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 M-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: fdoI
C;Superfamily: formate dehydrogenase gamma chain
C;Keywords: heterotrimer; NAD; oxidoreductase; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 211;
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5.1%; Score 82; DB 2;
Best Local Similarity 21.9%; Pred. No. 17;
Matches 44; Conservative 29; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 85.5; DB 1;
Pred. No. 0.95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1603 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVCLCCANIDIMISMMI-----HGYESWALHCH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 LOCIAGGOVLASWFRMVVDGAMFNORFIWYREVV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : : ||:| |:|
184 IMGMIGGKVSATW-----AKFHHP-KWYREVV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 GLPCSVGFTLIQEWVVPW--DMVLTREELVILRKC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 23.4%;
Matches, 36; Conservative 20
| | :: ||:
249 ESYKTIWMFWCRS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP: R09H10.5
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                        셤
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Nature 310, 207-211, 1984
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A;Reference number: A07394, MUDI:84270667
A;Reference number: A07394, MUDI:84270667
C;Superfentis: annotation; protein coding region
C;Superfentily: human herpesvirus 4 BHRP1 protein
C;Superfentily: human herpesvirus 4 BHRP1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CMHVCLCCANIDIMTS----MAIHG-----YESWALHCHCSSPGSLQCIAGGQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 VLASWERMVVDGAMENORFIWYREVVNYNMPKEVMFMS----SVFWRGRHLIYLRLWYD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 VLIAASTLLIVAASFERVICSLKSSIOFSPORRFLFISIVGACALFWKGSVFFELEL--- 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EINDICAEDP---PQADAFRMILIVIIGTVVCSLGI-----VLNTFLLLSLRRLDVFRS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETRATILEDHPLLPECNTLTMHNVSYVRGLPCSVGFTLIQEWVVPWDMVLTREELVILRK 95
                                                                                                                                                                                                                                                                                                                                                                                                                 N-----IDIMISMMI---HGYESWALHCHCSSPGSLQCIAGGGVLASWFRKVVDGAMFN 155
                                                                                                                                                                                                                                                                                                                                       59 VS------YVRGLPCSVGFTLIQEWVVPWDMVLTREELVILRKCMHVC--LCCA 104
                                                                                                                                                                                                                                                                                                                                                                              ---CMHACRILCCN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GG-----WSTLIEDNIPGS 161
                                                                                                                                                                                                                                                                                     24 TLHPVLELAARETPL---RLSPEDT----VVLRYHVLLEEIIERNSETFTETWNRFITHT 76
                                                                                                                                                                                                                                                                 --NTLIMHN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 NILYLFLLACLDILVELCFMLIFPASLVWDYFRVELLYTCWHFYIKYVS-----TVGQ
                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
5.5%; Score 87; DB 2; Length 494;
Best Local Similarity 20.2%; Pred. No. 1.7;
Matches 51; Conservative 40; Mismatches 96; Indels
                                                                                                                                                                                   Length 191;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                   11 TLRPIRSRLSRRIPYSRDRLPPFETETRATILEDHPLLPEC--
                                                                                                                                                                                           DB 1;
                                                                                                                                                                                       Query Match

5.6%; Score 88.5; DB

Best Local Similarity 23.3%; Pred. No. 0.45;
Matches 49; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 QSTPYXVVDLSVRGMLEASEGLDGW-IHQQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 QRFIWYREVVNYNWPKEVMFMSSVFMRGRH 185
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s elegans	C. Access C. Access A. Yaudin Submittee A. Access A. Acc	RESULT 11 Tybothetical protein W06F12.2a - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Accession: Ty6242 S; Lloyd, C. Submitted to the EMBL Data Library, December 1996 A; Reference number: Z20179 A; Reference number: Z20179 A; Residues: Ta6242 A; Residues: 1-562 <will> A; Residues: 1-562 <will> A; Residues: 1-562 <will> A; Residues: 1-562 <will> A; Residues: Caenore: EMBL: Z83244; PIDN: CAB54314.1; GSPDB: GN00021; CESP: W06F12.2a A; Genetics: C; Genetics: A; Genetics: A; Map Position: 3 A; Introns: Z3/3; 75/1; 153/3; 201/1; 214/1; 283/1; 305/3; 332/2; 555/3</will></will></will></will>
OY 64 GLPCSVGFTLIQEWVVPWDMVLTREELVILRKCMHVCLCCANIDIMT 110 DD 1029 TSGCKXEXIMAL	frican e_revis 31473 7, 307 ion in MUD:93 MUD:93 9; NID:; i Batn ii Batn iii	GVPEG-MILRPITSRIJVE 33; Mismatches 94; Indels 117; Gaps 13; GVPEG-MILRPITSRIJVE

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A;Genome: mitochondrion
A;Genome: code: SGC1
A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Superfamily: NADH dehydrogenase (upiquinone) naD; oxidative phosphorylatio
                                           E2 protein - human papillomavirus type 30
C; Species: human papillomavirus type 30
C; Species: human papillomavirus type 30
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C; Accession: S36506
R; Description: Primer directed sequencing of human papillomavirus types.
A; Reference number: S36406
A; Accession: S36506
A; Acce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 NY-----NMPKEVMFMSSVFMRGRHLIYLRLWYDGHVGSVVPAMSFGYSA---LHCGI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 KTEYKVEEWILKDVCENMWHTAPRQCFKKSGKRIEVWF----DGKKDNRTEYVVW--QWV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 IQEWVVPWDMYLTREELVILRK----- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 FCLANSNYERIHSRIMILPGGLQVFL--PLMASWWLLA------SLINLALP 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 K-----EVMEMSSVF------MRGRHLIYLRLW-------YDGHVGSVVPAM 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 PIINLIGELLVVMSVFSWSNPTILLMGTNIVITALYSLYMLIMTORGKHTHHINNITPSF 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 WDMVLTR------BELVILRKCMHVCLCCANIDIMTS-------MMIHGYESWAL 122
Date: 14-Aug_1998 #sequence_revision 14-Aug-1998 #text_change 07-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 ---HOYESWALHCHCSS---PGSLQCI-AGGOVLASWFRMVVDGAMFN--ORFIWYREVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 IEDHIVYWKAV--RHENVYLYKARQNNITKLRHQVVPCLQVCKAKACVAIEIQWALESLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 WGMINTSSICLRQTDLKSLIAYSSVSHMALVIAAILIQTPWSYMGATALMIAHGLTSSML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HCHCSS------PGSLQCIAGGOVLASWFRMVVDGAMFNQRFIWYREVVNYNMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.9%; Score 78; DB 2; Length 378; Best Local Similarity 21.6%; Pred. No. 8.9; Matches 50; Conservative 27; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
5.0%; Score 79; DB 2; Length 459;
Best Local Similarity 19.5%; Pred. No. 8.8;
Matches 37; Conservative 29; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 TREHALMALH 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 SFGYS--ALH
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A; Molecule type: MRNA
A; Molecule type: MRD: GARC>
A; Molecule type: MRD: KR2405; NID: 9433817; PIDN: CAA44275.1; PID: 9433818
A; Cass-references: Exmal: X62405; NID: 9433817; PIDN: CAA44275.1; PID: 9433818
A; Cross-references: Exmal: Krainstate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Reywords: chromoprotein; eye; G protein-coupled.receptor; glycoprotein; lipoprotein; C; Reywords: chromoprotein estatus predicted <TM2>
F; 74.96, Domain: transmembrane #status predicted <TM4>
F; 114.14.10, Domain: transmembrane #status predicted <TM5>
F; 203-270, Domain: transmembrane #status predicted <TM5>
F; 203-230, Domain: transmembrane #status predicted <TM5>
F; 203-230, Domain: transmembrane #status predicted <TM7>
F; 204-230, Domain: transmembrane #status predicted <TM7>
F; 205-230, Domain: transmembrane #status predicted <TM7>
F; 206-2309, Domain: transmembrane #status predicted <TM7>
F; 206-2409, Distantification of the predicted <TM7>
F; 206-2409, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Archer, S.N.; Lythgoe, J.N.; Hall, L. Proc. R. Soc. Lond. B Biol. Sci. 248, 19-25, 1992
Proc. R. Soc. Lond. B Biol. Sci. 248, 19-25, 1992
A; Title: Rod opsin cDNA sequence from the sand goby (Pomatoschistus minutus) compared A; Title: Rod opsin cDNA sequence from the sand goby (Pomatoschistus minutus) compared A; Asécrence number: $40688; MUID:92396703
A; Accession: $40688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - finback whale mitochondrion C;Species: mitochondrion Balaenoptera physalus (finback whale, common rorqual)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 MMIHGYE-SWALHCHCSSPGSLQCIAGGQVLASWFRMVVDG------AMFNQ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 HAIMGVAFSWIMAATCAVP-----PLVGWSRYIPEGMQCSCGVDYYTRAEGFNNE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 SMHGYEVIGRIGCHVEGFFATIGGE-IALWSLVVLAVERWVV-----VCKPISNFRFTEN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 TMHNVSYVRGLPCSV-GF--TLIQEWVVPWDMVLTREELVILRKCMHVCLCCANIDIMTS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pain, rod - Pomatoschistus minutus
| Species: Pomatoschistus minutus
| Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                            65 SSKRISALIEGLEVIQVLCLIAAFFLVFASAAMIYGIHTWSKYLV---WPWFPVMLSSIL 121
                                                                                                                                                                                                                                                                                                                              . 135 -----IAGG----QVL---ASWFRMVVDGAMFNQRFIWYREVVNYNMPKEVMFMSSVF 180
                                                                                                                                                                                                                                                         6 CCCCSSKDAAITIGIWSLVYALASLLLFGWQTGVLN-HCRVVTWAQSNLQCEWDCPCVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98;
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19.9%; Pred. No. 6.6;
tive 31; Mismatches 76; Indels
                                                             Length 562;
                                                                                                                                                                                                   100 CLCCANID-----SSPGSLQC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 AT---LAYCIMWWGGDVRSYWLAIT------ILEIIVVFINIYC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 MRGRHLIYLRLWYDGHVGSVVPAMSFGYSALHCGILNNIVVLCCSYC 227
                                                                                                                                     48; Indels
                                                                    5.0%; Score 79.5; DB 2;
23.4%; Pred. No. 9.8;
tive 25; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 RFIWYREVVNYNMPKEVMFMSSVFMRGRHLIYLR-----
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Best Local Similarity 19.9
Matches 51; Conservative
                                                                                   5.0%
Best Local Similarity 23.4%
Matches 39; Conservative
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B58851
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A;Note: ND4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
190 -NESI-----YCPD------SVSSTLRSNVSPVETVVEYNTYQTPT 226
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4.9%; Score 77.5; DB 2; Length 459;
Best Local Similarity 24.1%; Pred. No. 12;
Matches 26; Conservative 14; Mismatches 37; Indels 3
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Search completed: June 23, 2000, 10:05:43. Job time: 1748 sec

37; Indels 31; Gaps

40 TILEDHPLLPECNTLTMHNVSYVRGLPCSVGFTLIQEWVVP----WDMVLTREELVILRK 95

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96 CMHVCLCCANIDIMTSMMIHGYESWALHCHCSSPGSLQCIAGGOYLAS 143

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	Title: Perfect 8 Sequence:	score:	US-09-21 1594 1 MTTSGN	-09-214-478-2 94 MITSGVPFGMILRPIRSRLS	PTRSRLS	RALLQHHRPILMHDYDSTPM 294	ALIGNMENTS
	coring	table:	BLOSUM62 Gapop 10.0	•	Gapext 0.5		34
	Searched:	<u></u>	83857 86	seqs, 304	30454973 residues		E454_ADE02 P03239; 21-IIII-1986 (Rel.
	Total num	number of	hits	satisfying	chosen parameter	ers: 83857	
	Minimum Maximum	DB sed] DB sed]	length: 0 length: 1	1000000			EARLY E4 34 KD PROHUMAN Adenovirus
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	Database		SwissProt_38	t_38:*			MEDLINE, 82059444. Herisse J., Rigolet M., Dupont de Dinechin S., Galibert F.; Herisse J., Rigolet M., Dupont de Dinechin S., Galibert F.;
	អ <u>ក</u> ខ្លួន	ed. d 1s	No. is the n greater than s derived by	the number of 1 r than or equal ed by analysis o	results predi to the score of the total	<pre>predicted by chance to have a e score of the result being printed, total score distribution.</pre>	RT "Nucleotide sequence of adenovirus 2 Una insquencia constant and the entire E4 region."; RT carboxylia region of the fiber protein and the entire E4 region."; RL Nucleic Acids Res. 9:4023-4042(1981). RL Nucleic Acids Res. 9:4023-4042(1981). CC -!- MISCELLANEOUS: FOUND IN ASSOCIATION WITH E1B 55 KD PROTEIN. CC -!- MISCELLANEOUS: FOUND IN ASSOCIATION WITH E1B 55 KD PROTEIN.
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EARLY E4 34 KD PROTEIN.

SEQUENCE FROM N.A. MEDLINE; 96327849.

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                                                                                                                                                          dEDLINE, 94076430.
Sprengel J., Schmitz B., Heuss-Neitzel D., Zock C., Doerfler W.,
Nucleotide sequence of human adenovirus type 12 DNA: comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
EARLY E4 30 KD PROTEIN.
Human adenovirus type 40.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                          encoding the entire region E4.";
Nucleic Acids Res. 18:3065-3066(1990).
-! SIMILARITY: BELONGS TO THE ADENOVIRUS E4 30 TO 34 KD PROTEIN
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hogenkamp T., Esche H.; "Nucleotide sequence of the right 10% of adenovirus type 12 DNA
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MEDLINE; 94087748.
Davison A.J., Telford E.A., Watson M.S., McBride K., Mautner V.;
"The DNA sequence of adenovirus type 40.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.9%; Score 874.5; DB 1; Length 291; 55.7%; Pred. No. 6.5e-78; Ive 52; Mismatches 67; Indels 1.
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CD1A07D37FBB5E96 CRC64; \
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291 AA; 34383 MW;
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                                                                                                                                                                                                                functional analysis.";
J. Virol. 68:379-389(1994).
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EMBL; X51800; CABS7854.1;
PIR; S33952; S33952.
PIR; S10867; S10867.
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Best Local Similarity 55.77
Matches 151, Conservative
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P36710;
P36710;
01-70N-1994 (Rel. 29, Created)
01-70N-1994 (Rel. 29, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
EARLY E4 34 KD PROTEIN.
Human adenovirus type 12.
Yiruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                          Javier R., Shenk T.;
Mammary tumors induced by human adenovirus type 9: a role for the viral early region 4 gene.";
Breast Cancer Res. Treat. 39:57-67(1996).
-! SIMHIGHRITY: BELONGS TO THE ADENOVIRUS E4 30 TO 34 KD PROTEIN
FAMILY.
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MOD JUD 26 09:10:39 2000

MOD JUD 241 RTRLMLRAVRIIAEETTAMLYSCRIEF

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RO P89083:
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Best Local Similarity 63.77
Matches 174; Conservative
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SEQUENCE

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SEQUENCE FROM N.A.

RESULT 3
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DT 01-JUN
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Query Match
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-!- SIMILARITY: BELONGS TO THE ADENOVIRUS E4 30
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SEQUENCE 257 AA;
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P03238;
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MEDLINE; 82059444.

Herisse J., Rigolet M., Dupont de Dinechin S., Galibert F.;

Herisse J., Rigolet M., Dupont de Dinechin S., Galibert F.;

Herisse J., Rigolet M., Dupont de Dinechin S., Galibert F.;

**Rucleotide sequence of adenovirus 2 DNA fragment encoding for the carboxylic region of the fiber protein and the entire E4 region.";

Nucleic Acids Res. 9:4023-4042(1981).

**Nucleic Acids Res. 9:4023-4042(1981)*

Nucleic Acids Res. 9:4023-4042(1981).

**AINTENTINE INTRONS IN THE CONTINENT STUDIES.**

**CODING REGIONS WERE ASSIGNED BY CORRELATING EM DATA, S1 DIGEST.**

CODING REGIONS WERE ASSIGNED BY CORRELATING EM DATA, S1 DIGEST.**

**STUDIES, AND THE CONSENSUS SEQUENCES FOR INTRON SPLICING.**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -21-JUL-1986 (Rel. 01, Created)
-21-JUL-1986 (Rel. 01, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
PROBABLE EARLY E4 17 KD PROTEIN (CONTAINS: E4
Human adenovirus type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human adenovirus type 2.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus
                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
EMBL; J01917; -; NOT_ANNOTATED_CDS. PIR; A03804; Q4ADB2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPILMHDYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.3%;
llarity 50.2%;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30157 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 706; DB 1; Length 25
Pred. No. 1.4e-61;
7; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2D5E41A9D7A1EBC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                       DIGESTION
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RESULT 6
E434_ADECT
ID E434_ADECT
AC P87568;
DT 15-DEC-1998
DT 15-DEC-1998
DT 15-DEC-1998
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Best Local Similarity
Matches 80; Conserv
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Best Local S
Matches 70
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Early prot
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campbell J.B., Zhao Y.;
Submitted (NOV-1996) to
-!- SIMILARITY: BELONGS
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
EARLY E4 30 KD PROTEIN.
Canine adenovirus type 2 (strain Toronto A 26-61).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              Early protein. SEQUENCE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U77082; AAB38735.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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108
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1 1 56 1.153 AA; 153 AA; 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVRGLPCSVGFTLIQEWVVPWDMVLTREELVILRKCMHVCLCCANIDIMTSMMIHGYESW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALHCHCSSPGSLQCIAGGQVLASW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVTHDMMLFKA--SRGERTVYSVCWEGG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NMPKEVMFMSSVFMRGRHLIYLRLWYDG
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                                                                                                                                                                                 NORFIWYREVVNYNMPKEVMFMSSVFMRGRHLIYLRLWY-----
                                                                                                                      KCMHVCLCCANIDIMISMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMF 154
NKKYMWYREFVNSSRPDEINYVGSIIFRNTHYIYFRLSFFRTVHKACMEATKRCINPELG
                                                                                      HC---CLAEA------QTWRVHCHCSNSLSLQCMASKHVVQKVIEDFIKGGAM
                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SPPVEQPQVGQQPVAQQLDSDMNLSELPGEFINITDERLARQETVWNITPKNM
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                AA;
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1:53
17404
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                                                                                                                                                                                                                                                                                                                                                                                                30014 MW;
                                                                                                                                                                                                                                                                                                     15.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the EMBL/GenBank/DDBJ
TO THE ADENOVIRUS E4 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ϋ́N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 331; DB 1;
Pred. No. 2.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLY 17 KD PROTEIN EARLY 10 KD PROTEIN; 1B3A657DAD8557CC (
                                                                                                                                                                                                                                                                               Score 253.5; DB 1;
Pred. No. 1.5e-17;
7; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   9C966CA011C2A745 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J databases.
30 TO 34 KD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mastadenovirus.
                                                 ----- DGHVG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76;
                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                         Gaps
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RESULT 8
E434_ADECC
, ID E434_ADECC
AC Q65962;
DT 15-DEC-1998 (
DT 15-DEC-1998 (
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Best Local Sim
Matches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 ONTLIMENVSYVRGLP--CSVGETLIQEWVVPWDMVLTREELVI-----LRKCM 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 CNAETTSHVTAVVRAPIFCNC-FALCLEIPILWDDLLYRHEKLLFGGFTCNGGAELILNS 69
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitites requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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E434_ADECR
                                                                                                                                                                                        230 --KAEERRQTALKQAMMYGR.247
                                                                                                                                                                                                                                                                                                                        209 SALHCGILNNIVVLCCSYCADLSEIRVRCCARRTRRLMLRAVR-----
                                                                                                                                                                                                                                                                                                                                                                 117 YLWYREFVNSSRPDEINYVGSIMFRNIHYIYFRLSFFSTVHQACMLAIQRCISPELGVVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y07760; CAA69046.1; -. Early protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morrison M.D., Onions_D.E., Nicolson L.;
"Complete DNA sequence of canine adenovirus
J. Gen. Virol. 78:873-878(1997).
-i- SIMILARITY: BELONGS TO THE ADENOVIRUS E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 97275900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canine adenovirus type 1 (strain RI261).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998
15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLY E4 31 KD PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 HYCLCCANIDIMISMMIHGYESWALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168
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                                                                                                                                                                                                                                      SCRTERRRQQFIRALLQHHR 282
                                                                                                                                                                                                                                                                        KSTY----NYWLVLKCKSCSLQNYCALKSCAFWVRSIIDRVLREVEKIPVVLHRTTS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCCLADA------QMWQVHCHCSDSLSLQCLSATQVLKEFLEEFVMGGFVNKK 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMLY -- SCRTERRRQQFIRALLQHHR 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
(Rel. 37, Created)
(Rel. 37, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 AA; 30737 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 252.5; DB Pred. No. 2e-17;
                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14B3DC9DCB1D2E15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADENOVIRUS E4 31 TO 34 KD PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                           265
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                                                                                                                                                                                                                                                                                                                        -IIAEETTAMLY 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
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RESULT 9

E434_ADEM1 STANDARD; PRT; 289 AA.

ID E434_ADEM1 STANDARD; PRT; 289 AA.

AC P23125;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PROBABLE EARLY E4 33 KD PROTEIN (ORF A/B PROTE
OS Mouse adenovirus type 1 (MAV-1).

CVITISES; GEDNA VITUSES, NO RNA Stage; Adenovir
RN []

RP SEQUENCE FROM N.A.

RX MEDLINE; 91082417.

RA MEDLINE; 91082417.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 91082417.
Ball A.O., Beard C.W., Villegas
"Early region 4 sequence and b:
mouse adenovirus type 1.";
Virology 180:257-265(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-gor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 KSTY----NYWLVLKCKSCSLQNYCALKSCAFWVRSIIDRVLREVEKIPVVLHRTTS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U55001; AAB05452.1; -. Early protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dragulev B.P., Sira S., Abouhaidar M.G., Can "Sequence analysis of putative E3 and fiber strains of canine adenovirus type 1."; Virology 183:298-305(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 248-265 FROM N.A. MEDLINE; 91272490. Dragulev B.P., Sira S., Abouh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Last annotation
EARLY E4 31 KD PROTEIN.
Canine adenovirus type 1 (strain CLL).
Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 FIWYREVVNYNMPKEVMEMSSVFMRGRHLIYLRLWYDGHVGS-----VVPAMSFGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campbell J.B., Zhao Y.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Campbell J.B., Zha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    --KAEERRQTALKQAMMYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCRTERRROOFIRALLOHHR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SALHCGILNNIVVLCCSYCADLSEIRVRCCARRTRRLMLRAVR-----IIAEETTAMLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLWYREFVNSSRPDEINYVGSIMFRNIHYIYFRLSFFSTVHQACMLAIQRCISPELGVVF
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70; Conserv
                                                                                                                                                                dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30822 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.7%;
26.9%;
                                                  Villegas P., Spindler K.R.; ce and biological comparison
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Pred. No. 3.1
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A/B PROT!
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ber genomic regions
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                                                  two isolates of
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tent is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I- MISCELLANEOUS: THIS PROTEIN IS THE PRODUCT OF TWO DIFFERENT I 'SPLICED FROM THE SAME PRIMARY TRANSCRIPT.
-I- SIMILARITY: BELONGS TO THE ADENOVIRUS E4 30 TO 34 KD PROTEIN FAMILY.
                                                                                                                                                                                                                                                    P48733;
01-FEB-1996
01-FEB-1996
15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 28
                                                                                                                                                                                                                                                                                                             BOVIN
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                 UROM_BOVIN
                                                                                                                                                                                                                                DMOD.
                                                                                                                                                                                                                                         UROMODULIN
                                                                                                                                              TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147
                                                                                                                                                                                  Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                        253
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                                                                                                                                       MEDLINE; 95143938.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPLTMS--ATLSRMDCCVGLPHCMGWLPSPVGAVAFVMEGALPIPWSYYLNSYDKHVLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L--DCLCLFPVTCYQSFTSYVTGDEVWSLHCHCGRQGSLQVGPRRLQCLAAAKVRELVVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVVDGAMFNORFIWYREVVNYNMPKEVMEMSSVFMRGRHLIYLRLWYDGHVGSVVPAM--
                                                                                                                                                                                                                                                                                                                                                         IPGFDIPRNRTERLRQRMLHRFYSYRTPIYRLTY 286
                                                                                                                                                                                                                                                                                                                                                                           -----LYSCRTERRROOFIRALLQHHRPILMHDY 289
                                                                                                                                                                                                                                                                                                                                                                                                   RIGQGVIFCESLISCYVVIVCQQCACPPTDAQVDHCMRLISFTIRRWQNLLIGRSGSSPI 252
                                                                                                                                                                                                                                                                                                                                                                                                                         SFGYSALHC-GILNNIVVLCCSYCA-DLSEIRVRCCARRTRRLMLRAVRIIAEETTAM--
                                                                                                                                                                                                                                                                                                                                                                                                                                              KFLLGTRENEYYPQYRVHANRYVNPGLEYVGSVWC-GKHFIYVRA--DGAEFARLKGLRA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 24.8
68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 AA;
                                                                                                                                                                                                                                        6 (Rel. 33, Created)
6 (Rel. 33, Last sequence update)
0 (Rel. 39, Last annotation update)
0 (Rel. 39, Last annotation update)
pRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP).
                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%;
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Pred. No. 5.8e-11;
3; Mismatches 120;
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as its content
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RESULT
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EAR_EBV P03182; 21-JUL-1986

STANDARD;

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PROSITE; PS000602; ZP_DOMAIN; 1.
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS00022; EGF_1; FALSE_NEG
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01187; EGF_CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; S75958; AAB33312.1; -. HSSP; P35555; 1EMO.
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CARBOHYD
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  219
                                           205
                                                                                                                                                                                                                                                                                                    48 LPECNTLIMHNVSYVRG------LPCSVGFTL-----IQEWVVPWDMVLTREEL
                                                                                                                                                                                                                   91
                                                                                                                                                                                                                                                              83
C--VPVLHCNTAAPMWLNGTHPSSDEGIVNRVACAHWSGDCCLWDA---PIQVKACA
                                                                                 VCVDPCQVHRILDEYWRSTEYGSG----YICDVSLGG-----WYRFVGQAGVRLPET
                                                                                                                                                                          --LSRCHALATCINGEGNYSCVCPAGYLGDGRHCEC-SPGSCGPGLDCVREGDAL----
                                                                                                                                                                                                                VILRKCMHVCLCCANIDIMTSMMIHGYESWALHCHCSSPGS----LQCIAGGQVLASWFR 146
                                                                                                                            MYVDGAMFNQRFIWYREVVNYNMPKEVMFMSSVFMRGRHLIYLRLWYD--GHVGSVVPAM 204
                                                                                                                                                                                                                                                           LDECAVLGAHNCSATKSCVNTLGSYTCVCPEGFLLSSELGCEDVDECAEPG------
                                           SFGYSALHC----
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EGF-LIKE 2,
EGF-LIKE 3,
EGF-LIKE 1,
EFF-LIKE 1,
EFF-LIKE 1,
EFF-LIKE 1.
EFF-LIKE 3,
EFF-LI
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Pred. No. 0.26
19; Mismatches
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PROSITE; PS5;
PROSITE; PS0;
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EMBL; V01555; -; NOT_ANNOTATED_CDS.
EMBL; M17293; AAA45875.1; -.
EMBL; A22899; CAA01838.1; -.
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Baer R., Bankler A.T., Biggin M.D., Deininger P.L., Fallow Baer R., Barkler A.T., Biggin M.D., Deininger P.L., Fallow Baer R., Barkler A.T., Budson G.S., Satchwell S.C., Seguin C., CTRÉNELLES., Barrell B.G.;

Tuffinell.P.S., Barrell B.G.;

TURENA sequence and expression of the B95-8 Epstein-Barr virus genome.", Nature-310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of an Epstein-Barr virus early gene encoding a second component of the restricted early antigen complex.",
Virology 160:151-161(1987).
-i- FUNCTION: INHIBITS APOPTOSIS.
-i- MISCELLANEOUS: EA-R IS PART OF THE RESTRICTED EA-COMPLEX.
-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                       105
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Pearson G.R., Luka J., Petti L., Sample J., Birkenbach M., Kieff E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE: 87284169.
Pfiltzner A.J., Tsai E.C., Strominger J.L., Speck S.H.;
"Isolation and characterization of cDNA clones corresponding to transcripts from the BamHI H and F regions of the Epstein-Barr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION OF PROTEIN. MEDLINE; 87321098.
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                                                                          59
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15-JUL-1998 (Rel. 36,
EARLY ANTIGEN PROTEIN
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                                      EHVDLDENSVELEIFHRGDE-SLGRAL--AWMA-W-------CMHACRTLCCN 118
                                                                                        TLHPVLELAARETPL----RLSPEDT-----VVLRYHVLLEEIIERNSETFTETWNRFITHT 76
                                                                                                            TLRPTRSRLSRRTPYSRDRLPPFETETRATILEDHPLLPEC-----NTLTMHN 58
                                                        protein;
                                                                                                                                                       l Similarity
49; Conserv
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191 AA;
 Conservative
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23.3%;
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Last annotation update)
R (EA-R) (NUCLEAR ANTIGEN).
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POTENTIAL.
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POTENTIAL.
POTENTIAL.
POTENTIAL.
ROTENTIAL.
ROTENTIAL.
ROTENTIAL.
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Pred. No. 0
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.12;
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                                                                                                                                                                                                           EMBL; U23808
PIR; S31473;
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01-APR-1993
15-JUL-1999
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P29403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differentiation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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162 RRESWILFLAGLTLSLLVICSYLFISRGRH
                              QRFIWYREVVNYNMPKEVMFMSSVFMRGRH
                                                               QSTPYYVVDLSVRGMLEASEGLDGW-IHQQ-
                                185
   191
                                                               -GG--
                                                           -WSTLIEDNIPGS 161
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Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                            25, Created)
25, Last sequence update)
38, Last annotation update)
Xenopus embryos precedes
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photoreceptor

Batni S., Scalzetti L.C., Moody S.A., Knox B.E.;

"Characterization of the Xenopus rhodopsin gene.";

J. Biol. Chem. 271:3179-3186(1996).

-i- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALE.

LINKED TO CLS-RETINAL.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-i- SUBCELLULAR TOCATION: GENERAL PHOTORECEPTOR CELLS WHICH MED VISION IN DIM LIGHT.

-i- FISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MED VISION IN DIM LIGHT.

-i- PIM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUE RE BEOCGEDHODYLATER 17:307-318(1993). MEMBRANE PROTEIN.
PHOTORECEPTOR CELLS WHICH MEDIATES COVALENTLY

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THR RESIDUES MAY

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GCRDB; GCR_0487; -...
GCRDB; GCR_0497; -...
GCRDB; GCR_0972; -...
GCRDB; GCR_0972; -...
PRINTS; PR00238; OPSIN.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
PROSITE; PS00237; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
PFAM; PF00001; 7tm_1; 1.
Photoreceptor; Retinal protein; Transmen Phosphorylation; Lipoprotein; p CARBOHYD 2 2 BY CARBOHYD 15 15 BY DOMAIN 1 36 EX TRANSMEM 37 61 1 DOMAIN 62 73 CY TRANSMEM 74 98 2 n; Palmitate; G-p BY SIMILARITY. BY SIMILARITY EXTRACELLULAR. 1 (POTENTIAL). CYTOPLASMIC. 2 (POTENTIAL). Transmembrane; -protein Glycoprotein;

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                                                                                                                                                                            Limnocottus bergianus.
Limnocottus bergianus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygi1;
Eukaryota; Teleostei; Euteleostei; Acanthopterygi1; Percomorpha;
Neopterygi1; Teleostei; Euteleostei; Acanthopterygi1; Percomorpha;
Scorpaeniformes; Cottoidei; Abyssocottidae; Limnocottus.
"Molecular evolution of the cottoid fish endemic to Lake Baikal deduced from nuclear DNA evidence.";
deduced from nuclear DNA evidence.";
del. Evol. 8:415-422(197).
HOI. Phylogenet. Evol. 8:415-422(197).
HOI. PHYLOGENET ARE THE LIGHT-ABSORBING MOLECULES THAT -1- FUNCTION: VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
                                                                                                          SEQUENCE FROM N.A.
MEDLINE: 98086781.
Hunt D.M., Fitzgibbon J., Slobodyanyuk S.J.,
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                                                                                                Dulai K.S.;
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PALMITATE (BY SIMILARITY).

BY SIMILARITY.

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I -> M (IN REF. 2).

L -> A (IN REF. 2).

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3 (POTENTIAL).
CYTOPLASMIC.
4 (POTENTIAL).
EXTRACELLULAR.
5 (POTENTIAL).
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EXTRACELLULAR.
7 (POTENTIAL).
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CYTOPLASMIC.
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                                                                                                                     Bowmaker J.K.,
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DISULFID
BINDING
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DOMAIN
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Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision; Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.

NON_TER
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01-JUN-1994
01-JUN-1994
15-JUL-1999
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                                       _POMMI
OPSD_POMMI
P35403;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
OPSIN SUBFAMILY.
                                                                                                                                                                                                          MMIHGYE-SWALHCHCSSPGSLQCIAGGQVLASWFRMVVDG------AMFNQ 156
                                                                                                                           SFVIYMFIVHFLIPLSVIF----FCYGRLL
                                                                                                                                                     RFIWYREVVNYNMPKEVMFMSSVFMRGRHL
                                                                                                                                                                                HAIMGLAFSWVMALACAVP------PLVGWSRYIPEGMQCSCGVDYYTRAEGFNNE
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                                                                                                                                                                                                                                                                                                           Similarity
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                              Conservative
                                                         STANDARD;
    29,
38,
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, Last annotation v
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CYTOPLASMIC (P
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
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CYTOPLASMIC (I
4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                            Score 79; Pred. No.
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BY SIMILARITY.
RETINAL CHROMOPHORE (BY SIMILARITY).
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EXTRACELLULAR
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EXTRACELLULAR (POTENTIAL)
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                                                            PRT;
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                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                                                                                                                                                         Length 289;
                                                                                                                                                                                                                                                                                                  Indels
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Query Match
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Matches 51;
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CARBOHYD
BINDING
                                                                                                                                                         DISULFID SEQUENCE
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DOMAIN
I TRANSMEM 37
DOMAIN 62
TRANSMEM 74
DOMAIN 99
TRANSMEM 114
DOMAIN 134
TRANSMEM 153
TRANSMEM 157
TRANSMEM 203
DOMAIN 231
TRANSMEM 253
DOMAIN 257
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DOMAIN
TRANSMEM
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PROSITE; PS00238; OPSIN; 1.
PFAM; PF00001; 7tm_1; 1.
Photoreceptor; Retinal protein; Transmem
                                                                                                                                                                                                            CIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archer S. . Lyttgoe J.N., Hall L.;

*Rod opsin cDNA sequence from the sand goby (Pomatoschistus minutus) compared with those of other vertebrates.*;

Proc. R. Soc. Lond., B. Hall. Sci. 248:19-25(1992).

1- FUNCTION: VISUAL PIGHENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, COVALENTLY LINKED TO CIS-RETINAL.

1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

1- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X62405; CAA44275.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Perciformes; Gobiodei; Gobidae; Pomatoschistus.
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MISCELLANEOUS: THIS RHODOPSIN
SIMILARITY: BELONGS TO FAMILY
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PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
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                                                                                        Similarity
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                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipoprotein;
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                                                                      31;
                                                                                  Score 79;
Pred. No.
                                                                                                                                           RETINAL CHROMOPHORE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BB8CE379AFED4656 CRC64;
                                                                                                                                                                                                                                                       7 (POTENTIAL).
CYTOPLASMIC.
POTENTIAL.
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6 (POTENTIAL).
EXTRACELLULAR.
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5 (POTENTIAL).
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                                                                 ed. No. 2.1;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Glycoprotein; Vision;
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1 OF G-PROTEIN COUPLED RECEPTORS
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                                                                                                 1; Length 352;
                                                                   76;
                                                                 Indels
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                                                           Gaps
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Phosphorylation; Lipoprotein; Performance of the control of the co
                                                                                                                                                                  PROSITE; PS00237; G_PROTEIN_RECEPTOR; PROSITE; PS00238; OPSIN; 1.
                                                                                                                                           Photoreceptor;
                                                                                                                                                         PFAM; PF00001; 7tm_1; 1.
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Retinal protein; Transmembrane; Glycoprotein; n; Lipoprotein; Palmitate; G-protein coupled re 36 EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
1 (POTENTIAL).
2 73 CYTOPLASMIC (POTENTIAL).
98 2 (POTENTIAL).

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(POTENTIAL)

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EXTRACELLULAR (POTENTIAL).
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PRINTS; PRO0237; GPCRRHODOPSN
PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
                                                                             GCRDB; GCR_2445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archer S.N., Hirano J.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY LINKED TO CIS-RETINAL.
                                                                                                          EMBL; Y14484;
                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES VISION IN DIM LIGHT.
-1- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
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15-JUL-1998
15-JUL-1999
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O42604;
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Zeus faber (John Dory).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopteryqii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
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                                                                                                                                                                                                                                                                                                                                                                BE PHOSPHORYLATED.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Query Match 5.0%; Score 79; DB 1; Length 354; Pred. No. 2.1; Matches 53; Conservative 35; Mismatches 87; Indels 108; Gaps
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                                                                                                                        Db ... 202 SFVIYMFVCHFSIPLTIIF----FCYGRLLCAVKDAAAAQQESETTQRAEREVSRMVVIM 257
                                                                                                                                                                                                                                                                       ::55 TMHNVSYVRGLPCSV-GF--TLIQEWVVFWDMVLTREELVILRKCHHVCLCCANIDIMTS 111
                                                                                                                                                                                                         112 MMIHGYE-SWALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMF------NQ 156
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LIPID
SEQUENCE
                                                                                                                                                                                                                                                 98 SMHGYFYLGRTGCNLEGFFATLGGE-IALWSLVVLAVERWVV-----VCKPISNFRFGEN 151
                                                                                                                                                                                    152 HAVMGVSFTWLMACACSVP------PLFGWSRYIPEGMQCSCGIDYYTRAPGYNNE 201
314 RHCM----ITTLCCGKNP------FEEEEGASTTASKTE 342
                              226 -YCADLSEIRVRCCARRTRRLMLRAVRIIAEETTAMLYSCRTE 267
                                                            258 VIGFLICWLPYASVAWFIFTHQGSEFGPVFMTIPA----FFAKSSAIYNPMTYICMNKQF 313
                                                                                          188 ---YLRLWYD-------GHYGSYVPAMSFGYSALHCGILNNIYVLCCS--- 226
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177
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202 EXTRACELLULAR (POTENTIAL).

230 5 (POTENTIAL).

252 CYTOPLASMIC (POTENTIAL).

276 6 (POTENTIAL).

276 EXTRACELLULAR (POTENTIAL).

309 7 (POTENTIAL).

309 8 (POTENTIAL).

354 CYTOPLASMIC (POTENTIAL).

2 BY SIMILARITY.

359 BY SIMILARITY.

15 BY SIMILARITY.

15 BY SIMILARITY.

296 RETINAL CHROMOPHORE (BY SIMILARITY).

322 PALMITATE (BY SIMILARITY).

323 PALMITATE (BY SIMILARITY).

324 PALMITATE (BY SIMILARITY).

325 PALMITATE (BY SIMILARITY).
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Search completed: June 23, 2000, 10:14:48 Job time: 669 sec

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Title:
Perfect score:
Sequence:
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MTTSGVPFGMTLRPTRSRLS......RALLQHHRPILMHDYDSTPM 294
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sp_phage:*
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O9y748 emericella
O44515 caenorhabdi
O67148 aquifex aeo
O97180 drosophila
O23017 arabidopsis
O9w6a8 brachydanio
O23666 arabidopsis
O24416 fragaria an
O21884 caenorhabdi
O97285 plasmodium
O9y802 sparus aura
O22130 caenorhabdi
O18735 canis famil
O9yh05 diplodus an
O9yh05 diplodus an
                                                                                                                      071106 bovine aden 084211 porcine ade 09ytro porcine ade 071108 bovine aden p89027 ovine adeno
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ALIGNMENTS

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Query Match
Best Local Similarity
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071106; O7106;
01-AUG-1998 (TIEMBLIGL. 07, Created)
01-AUG-1998 (TIEMBLIGL. 07, Last sequence update)
01-NOV-1998 (TIEMBLIGL. 08, Last annotation update)
01-NOV-1998 (TIEMBLIGL. 08, Last annotation update)
ADENOVIRUS 3 COMPLETE GENOME.
Bovine adenovirus type 3 (Mastadenovirus bos3).
Puruses; dsDNA viruses, no RNA stage; Adenoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-WBR-1;
BAXI M.K., REDDY P.S., Z.
BABIUK L.A., TIKOO S.K.;
Virus Genes 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-WBR-1;
LEE J.B., BAXI M.K., IDAMAKANTI N.,
PYNE C. BABIUK L.A., TIKOO S.K.;
Virus Genes 0:0-0(1998).
                                                                                               STRAIN-WBR-1;
REDDY P.S., IDAMAKANTI N., ZAKHARTCHOUK A.N., BAXI M.K.,
PYNE C., BABIUK L.A., TIKOO S.K.;
PYNE C., BABIUK D.A., TIKOO S.K.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF030154; AAD09737.1; -.
SEQUENCE 219 AA; 26028 MW; 092D5CCD CRC32;
                                                                                                                                                                                                                                                                                                       MEDLINE; 98105785.

REDDY P.S., IDAMAKANTI N., ZAKHARTCHOUK A.N PYNE C., BABIUK L.A., TIKOO S.K.;

"Nucleotide sequence, genome organization, bowine adenovirus type 3.";

J. Virol. 72:1394-1402(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-WBR-1;
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                 ZAKHARTCHOUK A.N., BAXI M.K., LEE J.B.,
     Score 223.5; DB 12; pred. No. 7.7e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REDDY P.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219
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                                                                                                                                                                                                                                                                                                                                                                      transcription map of
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                                Length 219;
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Matches

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Query Match
Best Local S
Matches 45
       STRAIN-6618;
STRAIN-6618;
MEDLINE; 95351046.
REDDY P.S., NAGY E., DEF
"Sequence analysis of p
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01-NOV-1996 (TrEMBLrel 0
01-NOV-1996 (TrEMBLrel 0
01-NOV-1996 (TrEMBLrel 0
MASTADENOVIRUS 19.8 KDA POrcine adenovirus 3.
                                                                            SEQUENCE FROM N.A.
                                                                                                                    19.8 KDA POLYPEPTIDE. Porcine adenovirus 3.
                                                                                                                                             01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                                                                                        Viruses; dsDNA viruses,
                                                                                                                                                                                            Q9YTRO;
                                                                                                                                                                                                         Q9YTRO .
                                                                                                                                                                                                                                                                                              252 IIAEETTAMLYSCRTERRROOF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REDDY S., IDAMAKANTI N., DERBYSHIRE J.B., NAGY E.;
Submitted (JAN-1996) & the EMBL/GenBank/DDBJ databases.
EMBL; L43363; CAB24462.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-PAV-3;
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Q84211;
                                                                                                                                                                                                                                                                                                                                         195 --GHVGSVVPAMSFGYSALHC-GILNNIVVLCCSYCADLSEIRVRCCARRTRRIMLRAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSLQCRSAAVYFQGLVKQCVHGAQFDRVYWYFRRELSKLSSVFLAYVGSVYVNNVHLIYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPIPWKVIMPQED-----AHLTSCLCDYCLSFVIPGKRRSYYVHGEEWLYIHCHCPKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNLAPKRVKKHL---GLARLRDRFLERLARFREPVLFDRYD 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLWYDGHVGSVVPAMSFGYSALHCGILNNIVVLCCSYCADLSEIRVRCCARRTRRLMLRA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 AA;
                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                 ----YCDGDYANYIVLVCRRCHELSEPVARRCAQRLRHWLKLAAE 110
                     DERBYSHIRE J.B.;
f putative pVIII,
                                                                                                                                                                                                                                                                                                                                                                                                                                          11.3%;
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01, Last sequence update)
01, Last annotation update)
1 POLYPEPTIDE (ORF 8).
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                                                                                                     RNA stage;
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                                                                                                                                          Last sequence update)
Last annotation updat
                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 180; DB 12;
Pred. No. 2.1e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                        四3
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                                                                                                    Adenoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 163;
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                                                                                                   Mastadenovirus.
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Best Local Similarity

Matches 45; Conserv
                                       O71108 PRELIMINARY; ra., O71108;
O71108;
O71108;
O1-AUG-1998 (TrEMBLrel. O7, Created)
O1-AUG-1998 (TrEMBLrel. O7, Last sequence update)
O1-NOV-1998 (TREMBLrel. O8, Last annotation update)
ADENOVIRUS 3 COMPLETE GENOME.
Bovine adenovirus type 3 (Mastadenovirus bos3).
            SEQUENCE FROM N.A. STRAIN-WBR-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF083132; AAC99443.1; -. SEQUENCE 163 AA; 19786 MW; DAE89A1D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REDDY P.S., IDAMAKANTI N., SONG J.Y., LEE J.B., HYUN B.H., CHA S.H., BAE Y.T., TIKOO S.K., BABIUK L.A.; "Nucleotide sequence and transcription map of porcine adence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-0010, MEDITINE; 98014367.
REDDY P.S., IDAMAKANTI N., DERB'
                                                                                                                                                                                                                    111 AIGAQRRG-----
                                                                                                                                                                                                                                                                                                                                         141 LASWFRMVVDGAMFNQRFIWYREVVNYNMPKEVMFMSSVFMRGRHLIYLRLWYD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-6618;
                                                                                                                                                                                                                                        252 IIAEETTAMLYSCRTERRRQOF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE: 95407103.

REDDY P.S., TUBOLY T., DENNIS J.R., DERBYSHIRE J.B., NAGY E.;

"Comparison of the inverted terminal repetition sequences from five porcine adenovirus serotypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virus Res. [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 99058191.
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J.B., BAXI M.K.,
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                                                                                                                                                                                                                                                                                        --GHVGSVVPAMSFGYSALHC-GILNNIVVLCCSYCADLSEIRVRCCARRTRRLMLRAVR 251
                                                                                                                                                                                                                                                                                                                   RSIMREIIRGCEYNRIFWWFREAVNLPSVSRVXYVGSVMFRGAHLMYIKIMYDCDLKLL
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                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                 ----RKQQF 123
                                                                                                                                                                                                                                                                                                                                                                                        11.3%;
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Pred. No. 2.1e-11;
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porcine adenovirus type
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IDAMAKANTI N.,

REDDY P.S.,

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Best Local
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REDDY P.S., IDAMAKANTI N., ZAKHAMALLINGER, S., IDAMAKANTI N., ZAKHAMALLINGER, S.K., TIKOO S.K.;
PYNE C., BABIUK L.A., TIKOO S.K.;
CSPYNE C., BABIUK I.A., TIKOO S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 981
REDDY P.S.,
PYNE C., BAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-WBR-1;
BAXI M.K., REDDY P.S., Z.
BABIUK L.A., TIKOO S.K.;
Virus Genes 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYNE C.,
Virus Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P89027 PRELIMINARY; PRT; 220 AA. |
P89027;
D1-MAY-1997 (TrEMBLrel. 03, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update
E4.2 PROTEIN (25.6 KD PROTEIN).
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"Nucleotide sequence, genome organization, and bovine adenovirus type 3.";
J. Virol. 72:1394-1402(1998).
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                                                                                                                                                                                                                             MEDIINE; 96240641.

VRATI S., BROOKES D.E., STRIKE P., KHATRI A., BOYLE "Unique genome arrangement of an ovine adenovirus: 1 new proteins and proteinsse cleavage sites."; Virology 220:186-199(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovine adenovirus
   MEDLINE; 97271311.
XU Z.Z., HYATT A., BOYLE D.B., BOY
"Construction of ovine adenovirus
deletion of related terminal region
                                                                                                                                 SEQUENCE FROM N.A. STRAIN-OAV287;
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-OAV287
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272
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nes 0:0-0(1998).
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Pred. No. 2e
      region sequences.
                                        BOTH G.W.;
rus recombinants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5; DB 12;
2e-09;
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fication of
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Q9Y748;
Q1-NOV-1999
Q1-NOV-1999
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ EMBL; U40839; AAD45954.1; ...
SEQUENCE 220 AA; 25401 MW; DCAFF782 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 98277079.

KHATRI A., BOTH G.W.;

RIDENTIFICATION OF transcripts

adenovirus OAV287 ",

Virology 245:128-141(1998).
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[3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-OAV287;
                                                                                                                                                                                                                                                                                                                                                                                                           ANGERNAYR K., PARSON W., STOFFLER G., HAAS H.;
"Expression of atrC - encoding a novel member of the cassette transporter family in Aspergillus nidulans cycloheximide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Euascomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                               Biochim. Blophys. Acta 1453:304-310(1999).
EMBL; AF082072; AAD25925.1;
PROSITE; PS00211; ABC_TRANSPORTER; 2.
ATP-binding; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-FGSC A4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 HCHCSSPGSLQCIAGGQVLASWF-RMYVDGAMFNQRFIWYREV-VNYNMPKEVMFMSSVF 180
                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCHCNSPGSLQCLAAKSVLLSCENHMPV--TLFSERNVKTVPVCCNTWICCPLMFLGASQ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEIRVRCCARRIRRL-MLRAVRIIAEETTAMLYSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHKTHFYFLFSGVMEDDFSSKWYS---YQTVKRITFSETC-----
                                                                                    LIVLYRCRQ-CLPCSSGRFQQSHLIFQFPLPAMASEMLHKGNFWGIIYIVLAVSVLICYA 775
GLGFFFTVAASFLSGTYRSRYFAAMLNQDVSFFEEEDQSAGVMTGQLSTDPQRIEDLISL
                                                                                                                                    LVILRKCMHVCLCCAN-----
                                           G------GQVLASWFRMVVDGAMFNQRFIWYRE-----VVNYNM---PKEVMFMSSV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                  Similarity 21.4
50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99156773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QCISRFEKRFNFLR-------MLYCC
                                                                                                                                                                                                                                                                                                 1293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TIEMBLrel. 12, Created)
(TIEMBLrel. 12, Last sequence update)
(TIEMBLrel. 12, Last annotation updat
RTER PROTEIN ATRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%;
                                                                                                                                                                                                          5.6%;
                                                                                                                                                                                                                                                                                                 141984 MW;
                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 108; DB 12; Pred. No. 0.0011;
                                                                                                                                                                                    Score 90; DB
Pred. No. 0.65
%6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                      2D8E0446
                                                                                                                                         -IDIMTSMMIHGYESWALHCHCSSPGSLQCIA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1293
                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264
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                                                                                                                                                                                                                                                                                                        CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                       94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plectomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the
                                                                                                                                                                                                                                Length 1293
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                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -ELISIKCK-CSDT
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sensitive
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                                                                                                                                                                                         Gaps
         835
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SEQUENCE-FROM N.A.

STRAIM-BRISTOL N2;

RX. MEDLINE; 94150718;

RX. MEDLINE; 94150718.

RX. MEDLINE; 94150718.

RX. MEDLINE; 94150718.

RX. MEDLINE; 94150718.

RX. MEDLINE; 9415071.

RX. JCRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RX. JCRAXTON M., DEAR S., DI AMEXINS T., HILLIER L., JIER M., JOHNSTON L.,

RX. JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RX. JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RX. JONES M., KERSHAW J., KIRSTEN J., LAISTER N., JOHNSTON L.,

RX. JONES M., KERSHAW J., KIRSTEN J., LAISTER N., JOHNSTON N.,

RX. JONES M., SERSHAW J., KIRSTEN J., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RX. MELICAL M., SONNHAMMER E., STADEN R., SULSTON J.,

RX. MELICAL M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RX. METHERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RX. MELICAL M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RX. MELICAL M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RX. MELICAL M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RX. MELICAL M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RX. MELICAL M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RX. MELICAL M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RX. MELICAL M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RX. MELICAL M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RX. MELICAL M., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RX. MELICAL M., WEINSTOCK L., WILKINSON M., WALLEN M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
044515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WATERSTON R.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF038619; AAB92076.1; -
SEQUENCE 494 AA; 56780 MW; F59CC020 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATTUNG S., GOELA D., HI Submitted (DEC-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 044515;
                                                                                                                                         195
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                                                                                                                                                                                                                                                                     140
                                                                                                                                                                                                                                                                                                              104 NILYLELLACLDILVELCEMLIFPASLVWDYFRVELLYTCWHFYIKYVS-----TVGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                    96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239
                                                                                                              GHVGSVVPAMSFGYSALHCGILNNIVVLCCSYCADLSEIRVRCCARRIRRLMLRAVRIIA 254
                                                                                                                                                                                  VLIAASTLLIVAASFERYICSLKSSIQFSPQRRFLFISIVGACALFMKGSVFFELEL---
                                                                                                                                                                                                                                             VLASWFRMVVDGAMFNORFIWYREVVNYNMFKEVMFMS----SVFMRGRHLIYLRLWYD 194
                                                                                                                                                                                                                                                                                                                                                                               CMHVCLCCANIDIMTS---MMIHG-----YESWALHCHCSSPGSLQCIAGGQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EINDTCAEDP----PQADAFRMILIVIIGTVVCSLGI-----VLNTFLLLSLRRLDVFRS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETRATILEDHPLLPECNTLIMHNVSYYRGLPCSVGFTLIQEWVVPWDMVLTREELVILRK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARRTRRIMLR-----AVRIIA----EETTAMLYSCRTERRRQQFIRALL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLGFILLVVVNV-----LASCILALAVGWRLALVAIFGCLPPL---FLAGYVRVRLEITC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FMRGRHLIYLRLWYDGHVGSVVFAMSFGYSALHCGILNNIVVLCCSYCADLSBIRVR-CC: | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                       -QSLPHCPPFQNLRL-----DLSEI----TRRTKTYLIYGKLIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.5%;
20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HARPER M.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yda; Secernentea; Rhabditia; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 87; DB 5; Length 494; Pred. No. 0.45; Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                  156
                                                       248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               887
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                 RA RAC
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097180
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067148
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
MEDLINE; 99147028.
FELDMANN P., EICHER E.N., LEEVERS S.J., "Control of growth and differentiation"
                                                                           STRAIN=OREGON-R;
MEDLINE; 9914702
                                                                                                                                                                                                                                                                                                                                                                            RASGAP PROTEIN.
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          RASGAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      067148
067148;
01-AUG-1998
01-AUG-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=VF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aquifex aeolicus
Bacteria; Aquific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
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HAFEN E., HUGHES

GHES D.A.; RasGAP, a

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097180 PRELIMINARY;
097180;
01-MAY-1999 (TIEMBLrel. 10, C
01-MAY-1999 (TIEMBLrel. 10, L
01-NOV-1999 (TIEMBLrel. 12, I
                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LEN GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AE000720; AAC07109.1; -. SPA33D85 CRC32;
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DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBEI
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.";
                                                                                                                                                                                                                                                                                                                                        184 IWGMIGGKVSATW-----AKFHHP-KWYREVV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (Tremblrel. 07,
01-AUG-1998 (Tremblrel. 07,
01-NOV-1998 (Tremblrel. 08,
FORMATE DEHYDROGENASE GAMMA
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Last sequence update)
Last annotation update)
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Pred. No. 0.25
20; Mismatches
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Last annotation update)
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Mol. Cell. Biol. 19:1928-1937(1999).
EMBL; AJ012609; CAA10073.1; -.
HSSP; P20936; HEER.
PROSITE; PS00509; RAS_GTPASE_ACTIV_1; 1.
SEQUENCE 954 AA; 107950 MW; 0DB2B774 CRC32;
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01-JAN-1998 (TREMBLIGE). 05,
01-NOV-1999 (TREMBLIGE). 12,
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Paramatophyta; Magnollophyta; eudicotyledons;

Bukaryota; Tracheophyta;

Bukaryota; Trache
THEOLOGIS A.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ
EMBL; AC002376; AAB80622.1;
MENDEL; 25798; Arath;1088;25798.
PFAM; PF00544; pec_lyase; 1:
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OSBORNE B.I., VYSOTSKAIA V.S., TORIUMI M., YU G., OJI O., LIU
OSBORNE B.I., VYSOTSKAIA V.S., TORIUMI M., YU G., OJI O., LIU
LI J., HOANG L., BUEHLER E., CONWAY A.B., CONWAY A.R., DEWAR F
FING J., KIM C., KURTZ D., LI Y., SHINN P., SUN H., DAVIS R.W.
ECKER J.R., FEDERSPIEL N.A., THEOLOGIS A.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 1.4;
37; Mismatches
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Last sequence update)
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Q9W6A8;
Q1-NOV-1999 (TrEMBLrel. I:
Q1-NOV-1999 (TrEMBLrel. I:
Q1-NOV-1999 (TrEMBLrel. I:
BLUE-SENSITIVE OPSIN.
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023666;
023666;
01-JAN-1998
01-JAN-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIHTELIC T.S., DORO C.J., HYDE D.R.;
"Cloning and characterization of six zebrafish photoreceptor cDNAs and immunolocalization of their corresponding proteins. Vis. Neurosci. 0:0-0(1999).
EMBL; AF109372; AAD24755.1; -.
PROSITE; PS00238; OPSIN; 1.
SEQUENCE 354 AA; 39483 MW; 535F4C88 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostel; Euteleostel; Ostariophysl; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
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                                                                                                                                                                                                                       FSTIVFCYGQLLITLKLAAKAQADSASTQKAEREVTKMVVVMVFGF
                                                                                                                                                                                                                                                                                                                                                                         HCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFIWYREVVNYNMPKEVMFM---
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                                                                                                                                                                                                                                                                         --SSVFMRGRHLIYLRL---
                                                                                                                                                                                                                                                                                                                        -CILPWCMALAAGLPPLLGWSRYIPEGLQCSCGPDWYTTNNKFNNESYVMFLFCFCFAVP
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1 Similarity 24.1%;
40; Conservative 1
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A; 47770 MW;
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Last annotation update)
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Pred. No. 0.81
18; Mismatches
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0.81;
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RI lyase from
RL Plant Mol.
DR EMBL; U635
DR MENDEL; 26
EMBL; W635
CW Lyase
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Ouery Match
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Best Local S
Matches 35
                                                                                                                                       MENDEL; 200-
DFAM; PF00544; /
                                                                                                                                                                  strawberry ripening-specific cDNA with selfvase from higher plants.", Plant Mol. Biol. 34:867-877(1997).
EMBL; U63550; AAB71208.1; -
MENDEL; 26059; Frax; 1088; 26059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998
01-JAN-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                              Fragaria ananassa (Strawberry).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Fragaria.
                                                                                                                                                                                                                                                                     MEDLINE; 97435972.
MEDINA-ESCOBAR N., CARDENAS J.,
MUNOZ-BLANCO J.,
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                    Cloning, molecular characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PECTATE LYASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of the tobacco and Arabidopsis homologues of the pollen-expressed LaT59 gene of tomato."; Plant Mol. Biol. 34:809-814(1997).
EMBL: U83620; AAB69760.1; -
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core_eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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PFAM; PF00544; pec_lyase; 1.
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181 AA;
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                                                                                                                       ΑA;
                                                                                                                                                      pec_lyase;
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20088 |
                                                                                                                      45744 MW;
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Last sequence update)
Last annotation update)
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Pred. No. 0.43;
                                                                                                                    2B9944A0 CRC32;
                                                                                                                                                                                                                                                                                 MOYANO E., CABALLERO J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EF3426C6 CRC32;
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1 Similarity 47; Conserv

Conservative

25;

Score 82.5; D Pred. No. 1.1; 25; Mismatches

DB 10; 66;

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YREVVNYNMPKEVMFMSSVFM 181

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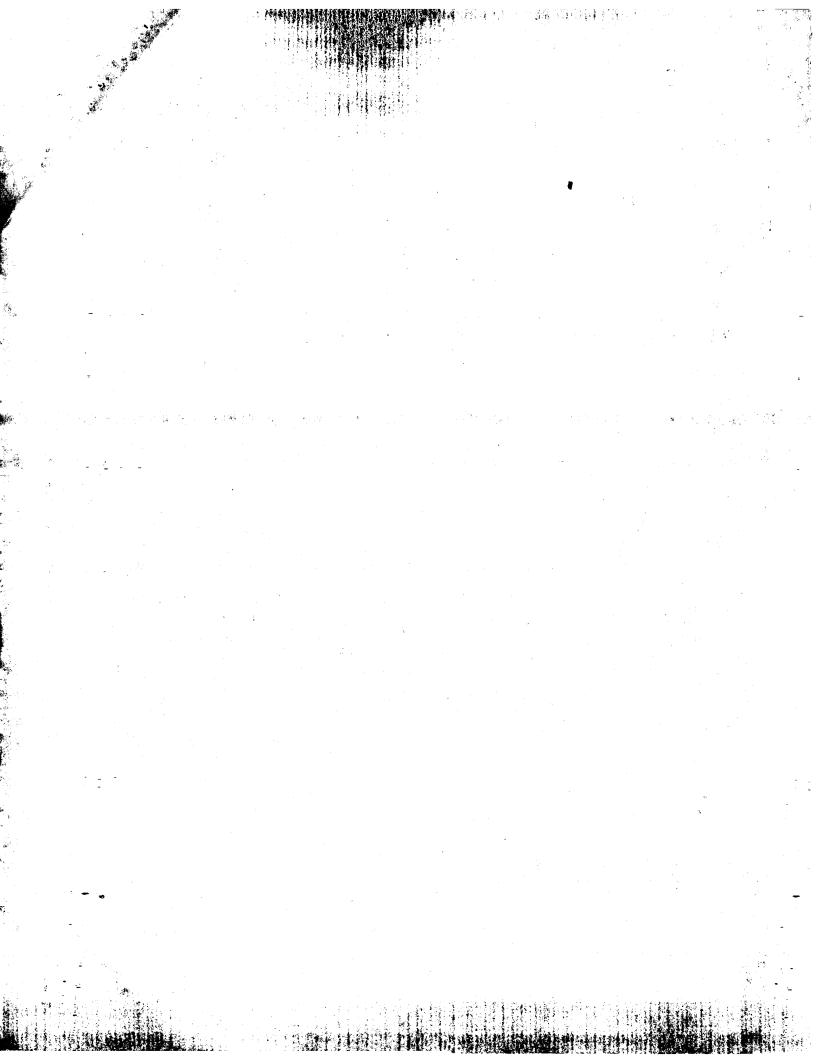
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BONFIELD J., BURTON J., CONNELL M., COPESY T., COOPER J., COULS
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LAOYD C., MCMCHRAY A., WORTINGE B., O'CALLAGHAN B.
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNK
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.
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Q21884;
Q1-NOV-1996
                                                                                                                                                                                                                                                  EMBL; Z77134; CABOO874.1; -. HSSP; P00750; ITPG. SEQUENCE 1603 AA; 175349
                                                                                                                                                                                                                                                                                              Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                               elegans.
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Rhabditina; Rhabditoidea;
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Caenorhabditis elegans.
Metazoa; Nematoda;
                                                                                                            972 GFSPDPSFDRFSRDLTYATHQQPVIHL---SSTLQSDPSIDVTSYDNNNNIAFTSLFTKR 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 94150718
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                                                     TSGCKYEYIMNQEYTCQSAGDTFTMETTITTNEVTIMRTQRAYCSDLIGCINGGIMLGGN 1088
CQCVNGYTS--LHCEVPTCQNGGSVVDFKCQCPSIYDG--
                     SMMIHGYESWALHCH----CSSPGSL-----QC--IAGGQVLASWFRMVVDGAMENQRFIW
                                                                                GLPCSVGFTLIQEW------VVPWDMVLTREELVILRKCMHVC----LCCANIDIM---T
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21.9%;
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                         Score 82; DB Pred. No. 5.7; Pred. No. 5.7;
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1136 --NEVETHDPREYNEQQIVEV 1154

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Query Match 5.1%; Score 80.5; DB 5; Length 433; Best Local Similarity 21.1%; Pred. No. 1.9; Matches 58; Conservative 49; Mismatches 89; Indels 79
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OLIVER K., BOWMAN S., HARRIS D., LAWSON D., QUAIL M., BARRELL B.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBU databases.
EMBL; AL034559; CAB39031.1; -.
PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
ATP-binding; RNA-binding; Helicase.
SEQUENCE 433 AA; 49413 MW; C419B9EF CRC32;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WOV-1999 (TrEMBLrel. 12, Last annotation update)
pFC0915W PROTEIN.
316 KITELGYS-----SFYIHARMSQTHRNRVFHDF 343
                                                                                                      256 ETTAMLYSCRTERRRQQFIRA-LLQHHRPILMHDY 289 : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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karyota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Search completed: June 23, 2000, 10:07:44 Job time: 947 sec



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Listing first 45
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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2: pir2:
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109.534 Million cell updates/sec
 99.5
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H70233
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0 注 物点:	0; Gaps ,	Length 114;	Score 618; DB 1; pred. No. 7.1e-60 1; Mismatches	99.5%; 99.1%; Live	va	imilarit ; Conse	Query Match Best Local Similarity Matches 113; Conser	Query Ma Best Loo Matches	
1 Total			E4 13K protein	early:		: 95.0-96.0 adenovirus rly protein	A;Map position: 95.0-96.0 C;Superfamily: adenovirus C;Keywords: early protein	A; Map posit C; Superfami C; Keywords:	
tion st	and S1 digestion	EM data	s assigned by correlating	n was	R> protein	pe: DNA -114 <hef probable</hef 	is 1t	A; Molecule ty A; Residues: 1 A; Note: this	
carboxylic	for the	fragment encoding	1981 adenovirus 2 DNA :82059444	042, of MUID	sequence A93733;	Rigolet Res. 9, otide se ober: AS	<pre>k; HeTiSSe, J.; kigolet, m.; bupo Nucleic Acids Res. 9, 4023-4042, A; Title: Nucleotide sequence of A; Reference number: A93733; MUID A; Accession: A03806</pre>	R; Heris Nucleio A; Titlo A; Refe	
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Db --- 1 MPIPCIPPPPVSRDTAACIAWIGLAHASCVDTLRFIKHHDLKITPEAEYILASLREWIYF 60
                                                                                                                   A; Reference number: S29651; MUID:93160241
A; Accession: S29651
                                                                                                                                                            R;Pearson, J.A.; Tyler, M.I.; Retson, K.V.; Howden, M.E.H. Biochim. Biophys. Acta 1161, 223-229, 1993
A;Title: Studies on the subunit structure of textilotoxin, a ces of all the subunits.
                                                                                                                                                                                                                                                              textilotoxin chain A - eastern brown snake
C;Species: Pseudonaja textilis (eastern brown snake)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #
                                                                                                                                                                                                                                                                                                                                             RESULT
S29651
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A; Molecule type: DNA
A; Residues: 1-373 <WHI>
A; Cross-references: GB:AE001952; GB:AE000513; NID:g6458725; PIDN:AAF10581.1; PID:g645873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: F75449

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250

A;Accession: F75449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dGTP triphosphohydrolase-related protein - Deinococcus radiodurans (strain C;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-120 <SPR>
A;Cross-references: EMBL:X73487; NID:g313361; PIDN:CAA51902.1; PID:g313387
C;Superfamily: adenovirus early E4 13K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                      Residues: 1-118 <PEA>
                                                                                                                                                                                                                                                    Accession: S29651
                                    Superfamily:
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Best Local S
Matches 43
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 YYNYYTER 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 QNECVGWL-----GVAYSAVV--DVIRAAAHEGVYIEPEARGRL----DALREWI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVLPALPAPPVCDSQNECVGWLGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREWIYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
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40.2%; Pred. No. 8.4e-20;
tive 23; Mismatches 41
                                  A2
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no. 0.31;
no. 0.31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                                                                  #text_change 17-Mar-1999
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               A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; C;Superfamily: immunoglobulin V region; immunoglobulin homolog C;Keywords: heterotetramer; immunoglobulin
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                                                                                      A; Molecule type: mRNA
A; Residues: 1-155 <CHA>
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-129/Domain: immunoglobulin homology <IMM>
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A;Description: Dominance of clonotypic patterns and variable A;Reference number: S31509
A;Accession: S31511
                                                                                                                                                                                                                                       C;Accession: S31511
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M. submitted to the EMBL Data Library, December 1992
                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
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C;Acce
A; Status: preliminary
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C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
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A; Residues: 1-1232 <BUL>
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cobalamin biosynthesis protein N homolog - Methanococcus jannaschii
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Best Local :
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 -VDVIRAAAHEGVYIEPEARGRLDALREWIYYNYTERSKRRDRRRRSVCHARTWECERK 88,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 CDSQNECVGWLGVAY------SAVVDVIRAA-AHEGVYIEPEARGRLDALREWIYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYEEPRPMPWQGIYYKGKYFETLDD-----YLNYLKELGRDLDKPIIGVLFYRNWFVANN 198
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35; Conserv
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23.8%;
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29.0%; Pred. No. 0
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Pred. No. 8.5;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223
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PID: g33095

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submitted to the EMBL Data Library, August 1992
A; Reference number: $24675
A; Accession: $24675
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1799 (SEN)
A; Cross-references: EMBL:214256; NID:g59257; PIDN:CAA78622.1; PID:g59258
A; Cross-references: EMBL:214256; NID:g59257; PIDN:CAA78622.1; PID:g59258
C; Superfamily: POZ domain homology
                                                                                                                                                                                                                                                                      C; Superfamily: PC F; 12-115/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                              platelet-activating factor-acetylhydrolase (EC 3.1.-.-) precursor N; Alternate names: PAF-acetylhydrolase
                                                     A; Experimental source: liver
C; Comment: This enzyme converts platelet-activating factor to an inactive metabolite ly:
C; Keywords: glycoprotein; hydrolase
C; Keywords: glycoprotein; hydrolase
                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-436 < KAR1>
                                                                                                                           A; Molecule type: protein
A; Residues: 123-129; 134-139; 208-217; 258-264; 332-337; 341-345; 346-361; 373-384; 385-392
                                                                                                                                                                                                                                                      A; Accession: JC5021
                                                                                                                                                                   A; Accession: PC4207
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Ectromelia virus
Date: 20-Feb-1995 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                    Species: Cavia porcellus (guinea pig)
Date: 30-Sep-1993 #sequence_revision 21-Jan-1997
                                                                                                                                                                                     Cross-references: DDBJ:D67037; NID:g1644228; PIDN:BAA11054.1; PID:d1011714; PID:g1644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 MYMRNIPTLITTDAFKNAV-----FEILLDII--STNDGEYVYREGY-KVTILLKWLDY 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 VYHDTNYN 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 FCFRK-----YDYVRRSIWHDTTTNTIS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 QPPGKG-----LEWIGYIYYTGSATYNPPLKSRVTISVDTSKNQFSLKVSSVTAADTAVY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 EPEARGRLDALREWIYYNYYT--------ERSKRR-DRRRRSVCHART--W 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYITEEQLLCILSCIDIQNLDKKSRLLLYSNTTINMYSSCVKFLLDNKQNRNIIPRQLCL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IWHDTTTN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYYTERS-----KRRDRRRRSVCHARTWF-----CFR-----KYDYVRRS--- 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Conservative
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signal sequence #status predicted <SIG>
ct: platelet-activating factor-acetylhydrolase #status predicted
inding site: carbohydrate (Asn) (covalent) #status predicted
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28.1%;
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Pred. No.
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                        #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         guinea pig
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cell surface antigen 4F2 heavy chain - Rattus leucopus N;Alternate names: neutral amino acid transporter system L-linked protein C;Species: Rattus leucopus C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 23-Jul-1999 C;Accession: S64702; S57719 R;Broeer, S.; Broeer, A.; Hamprecht, B. Blochem, J. 312, 863-870, 1995
                                                                                                                                                       Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987
A;Accession: B70834
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C; Keywords: surface
                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Rv0383c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-527 <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S64702; MUID: 96128073
A; Accession: S64702
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A; Title: The 4F2hc surface antigen is necessary
                                                                                                                                                                                                                                                                                                                                     C; Accession: B70834
R; Cole, S.T.; Brosci
                                      A;Cross-references: GB:AL021931; GB:AL123456; NID:g3261526; A;Experimental source: strain H37Rv
                                                                                         A; Molecule type: DNA
A; Residues: 1-284 <COL>
                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X89225; NID:g895883; PIDN:CAA61509.1; PID:g895884
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Best Local S
Matches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 RRSVC-HARTW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 VGWLGVAYSAVVDVIRAAA------HEG-----VYIEPEARGRLDALREWIY 59
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Rv0383c
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                                                                                                                                                                                                                                                                                                              Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
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Pred. No. 17;
10; Mismatches
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Pred. No.
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                                                                       PIDN:CAA17389.1;
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                                                                       PID:e125
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60 YNYYTERSKRRDRR

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A; Molecule type: DNA
-A; Residues: 1-1083 <ROU>
-A; Cross-references: EMBL: AC003974; NID: g2914688; PID: g2914695
-A; Experimental source: cultivar Columbia
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                                                                                                                                                                 A; Note: F24L7.8
                                                                                                 Best Local :
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                                                                                                                                                                                                                                                                                                                     R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, submitted to the EMBL Data Library, February 1998 A;Description: Arabidopsis thaliana chromosome II A;Reference number: Z14204 A;Accession: T00790
                                                                                                                                                                                                                                                                                                                                                                                                                  ubiquitin-specific proteinase homolog F24L7.8 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Species: Arabidopsis thaliana (mouse-ear cress) # 12-Feb-1999 # text_change 30-Apr-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; anonymous,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          valy1-tRNA synthetase (vals) PAB1255 - Pyrococcus abyssi (strain Orsay)
C; Species: Pyrococcus abyssi
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G75014
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                                                                                                                                                                                                                                                                                                      Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                   Genetics:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 24-Nov-1999
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Best Local Similarity
            931
                                       14 SQNECVGWLGVAYSAVVDVIRAAAHEGVYI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485 EHNFPTA-----LRPQGTDIIRTWAFYTIFRTFKLTGKKPWKDIVIN 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435 PPVEKCPVCGAEIEPVTDVLDCWVD---SSITPLIITRWHEAIKGDEEA------KKWF 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 YYNYYTERSKRRDRRRRSVCHARTW---FCFRKYDYVRRSIWHDTTTN 103
                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
     SDNECENWEDLAVDSEEVIVKRDARKKVLINKAPPVLTIHLKRFSQDARGRVSKLSGHVD 990
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18; Conserv
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23.1%;
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Pred. No.
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Pred. No. 15;
9; Mismatches
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                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                       ----EPEARGRLDALREWIY 59
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ERSKRRDRRRRSVCHARTWFCF-----RKYDYVRRSIWHDTTNTISVV

108

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63

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13

Conservative

17;

Mismatches

48;

21;

Gaps

DSQNECV----GW----LGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREWIYYNYYT 64

DGHIVCVCSIAGWSGETMGLSYCTSKFAVRGAM-ESLQMELRDRG-LEGIKTTTLYPYFA

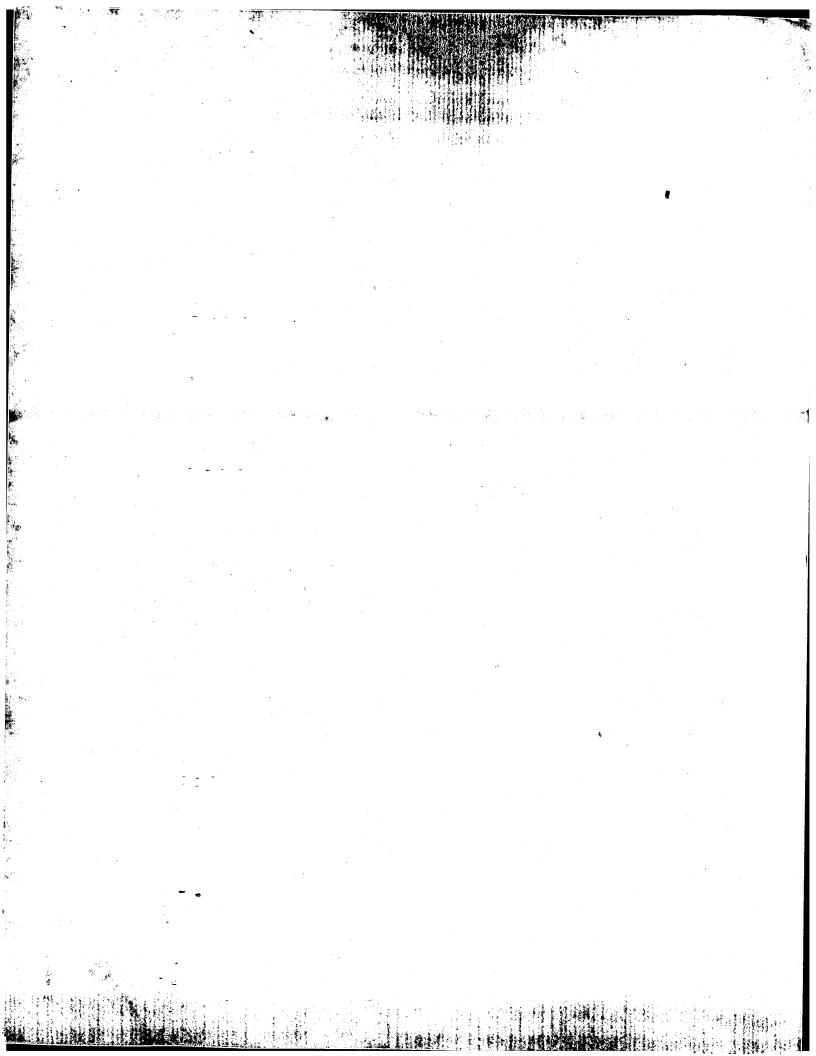
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-264 <BENA
A;Cross-references: EMBL:U49829; NID:g1203924; PID:
                                                                                                     A; Gene: CESP:F27D9.6
A; Introns: 28/2; 57/3;
                                                                                                                                                                                                                                                                            A; Reference number: Z18473
A; Accession: T16188
                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, February 1996 A; Description: The sequence of C. elegans cosmid F27D9
                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16188
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A;Residues: 1-1695 <RES>
A;Cross-references: GB:D29951; NID:g976234; PIDN:BAA06221.1; PID:g976235
A;Cuperfamily: Kinesin-related protein unc-104; Kinesin motor domain home
C;Keywords: P-loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: A55921
R;Okada, Y.; Yamazaki, H.; Sekine-Aizawa, Y.; Hirokawa, N.
Cell 81, 769-780, 1995
A;Title: The neuron-specific kinesin superfamily protein KIFyA is a unique monomeric...
A;Reference number: A56921; MUID:95292344
                                                                                                                                                                                                                                                                                                                                                                                  R; Bentley,
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F;97-104/Region: nucleotide-binding motif A (P-loop)
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F27D9.6 - Caenorhabditis elegans
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Score 63.5;
Pred. No. 17;
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                       2;
                       Length 264;
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64 RTPMILENNMRPTC---TWFPFMSIRSCSKRMVDSILKEKVHAFVPSYITLI 112

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Page 5
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"Db : 354 WEGRPRSIVEGVCYRYDPSNDTIDSIKAVPKENILATFKGN----WRNCIFYSYAGESE 408
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Search completed: June 23, 2000, 10:05:47 Job time: 1752 sec
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Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
Accession: T40584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: EMBL:AL035216; PIDN:CAA22812.1; GSPDB:GN00067; SPDB:SPBC646.08c Experimental source: strain 972h-; cosmid c646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. bmitted to the EMBL Data Library, January 1999 Reference number: Z21938 Accession: T40584
                                                                                                                                                                                                                                                                                           21 WLGVAYSAV-------VDVIRAAAHEGYYIEPEARGRIDALREWIYYNYYTERS 67
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Matches 725; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene: SPDBESPBC646.08c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA
Residues: 1-516 <SEE>
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                                                                                                                              409 SRMIVDINELDIVHKRCPPLDKQFPFESRKIWFPVTHN---ILAKHYTQ 454
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22.9%; Pred. No. 34;
tive 14; Mismatches 47; Indels 23; Gaps
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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621
1 MVLPALPAPPVCDS
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Query
Match
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                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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E413_ADE02
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PAPA_CAVPO
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DAPF_STRCO
CEGT_HUMAN
FSD3_DAUCA
DYHC_YEAST
MGG_RAT
EXG_YARLI
STAR_DROME
UL87_HCMVA
VP9_WTV
VATR_EALIV
VATR_RHISN
UL66_HCMVA
VIF_HV2ST
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LCB3_ROBPS
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LCB3_ROBPS
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MGG_BOYN
VP9_WTVNJ
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p36709 human adeno
p3026 pseudonaja
p17263 rhizobium m
p42546 bacteriopha
o70693 c platelet-
o12756 homo sapien
p33173 mus musculu
o61885 mus musculu
o69969 streptomyce
o16739 homo sapien
906364 daucus Garo
936022 saccharomyc
9360245 rattus norv
912725 yarrowia 11
942519 drosopiila
p16730 human cytom
p1236 wound tumor
p31598 salmonella
p16793 human cytom
p16716 capripoxvir
p55726 rhizobium s
p16822 human cytom
p16822 human cytom
p20878 human immun
p22567 pseudomonas
p21921 pseudomonas
p21921 pseudomonas
p21921 pseudomonas
p21927 sciara copr
083466 treponema p
p34367 caenorhabdi
p01744 homo sapien
p55803 bos taurus
p31611 wound tumor
                                                                                                                                                                                                                                                                                                                                                                            Description
    8
    Viruses; dsDNA Viruses, no kNA stage; Adelloviridae; Mastadellovirus:
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ש ב	.YSAVVDVIRAAAHEGVYIEPEARGRLDAL.	2FB72749D56345 2FB72749D56345 re 618; DB 1; d. No. 1e-61; Mismatches	format format. The long moved. (See h).	echin DNA f	pdate) update) Adenoviridae;	ENTS	didning 0332
20 AA. date) update) Adenoviridae;	SVYIEPEA (SVYIEPEA TTINTISV 	7 CR Le	duced s and are n its c Usage tp://w	, Ga ment e en ASSI			
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Best Local S
Matches 43
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Pearson J.A., Tyler M.I., Retson K.V., Howden M.E.H.;

"Studies on the subunit structure of textilotoxin, a potent

"presynaptic neurotoxin from the venom of the Australian common bro

snake (Pseudonaja textilis). 3. The complete amino-acid sequences
  MEDIINE; 88000715.

Tyler M.I., Barnett D., Nicholson P., "Studies on the subunit structure of t neurotoxin from the venom of the Austr
                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudonaja textilis (Eastern brown snake).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PA2A_PSETE STANDARD; PRT; 118 AA. P23026; 01-NOV-1991 (Rel. 20, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) PHOSPHOLIPASE A2 HOMOLOG, TEXTILOTOXIN A CHAIN TRACKET PROPERTY STARKE)
                                                                                                         TISSUE-VENOM;
                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                             TISSUE-VENOM,
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  Acanthophiinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 120
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Nucleic Acids Res. 18:3065-3066(1990).
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Hogenkamp T., Esche H.;
"Nucleotide sequence of the right 10% of adenovirus type 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 90272430.
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SEQUENCE FROM N.A.
MEDLINE; 94076430
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J. Virol. 68:379-389(1994).
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$10865; $10865.
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X51800; CAB57853.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                             Pseudonaja.
                                                                                                                                                                    Acta 1161:223-229(1993).
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Pred. No. 1e-20;
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       Australian
                        textilotoxin,
                                                   Spence I.,
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Query Match
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(L Biochim. Blophys. Acta 915:210-216(1987).

(L BIOCTION: POTENT PRESYNAPTIC NEUROTOXIN POSSESSING PHOSPHOLIPASE ACTIVITY. SUBUNIT A IS LETHAL TO MICE AT 4 MG/KG (I.V.). IT IS ESSENTIAL FOR THE NEUROTOXICITY OF TEXTILOTOXIN. SUBUNIT A CESSENTIAL FOR THE NEUROTOXICITY OF TEXTILOTOXIN. SUBUNIT A POSSESSES A LOW PHOSPHOLIPASE ACTIVITY.

(C POSSESSES A LOW PHOSPHOPASE ACTIVITY.

(C -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE CACTIVITY PHOSPHOTIVE HOLINE + H(2)0 - 1-ACYLGLYCERYL-COMPACTURITY: PHOSPHOTIVE NOTONICAL ENTRY LINKED SUBUNITS A, B, COMPACTURITY PHOSPHOTIVE NOTONICAL SUBUNITS.

(C -1- SUBUNIT: PENTAMER OF THREE NON-COVALENTLY LINKED SUBUNITS. A, B, CAND C, AND TWO LDENTICAL COVALENTLY LINKED SUBUNITS.

(C -1- MINCELLANGUS: ALL SUBUNITS ARE NECESSARY FOR MAXIMUM LETHALITY.

(C -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. 9
                                                                                                                                                                                                                                                                     RP54_RHIME STANDARD; PF
P17263; Q59751;
01-AUG-1990 (Rel. 15, Created)
15-FEB-2000 (Rel. 39, Last seque
15-FEB-2000 (Rel. 39, Last annot
RNA_POLYMERASE SIGMA-54 FACTOR (
MEDLINE; 89197760.

Albright L.M., Ronson C.W., Nixon B.T., Ausubel F.M.;

"Identification of a gene linked to Rhizobium meliloti ntrA whose product is homologous to a family to ATP-binding proteins.";
                                                                                                               MEDLINE; 87222158.
Ronson C.W., Nixon B.T., Albrigh
"Rhizobium mellioti ntrA (rpoN)
metabolic functions.";
                                                                                                                                                                                                            Rhizobium mellloti.
Bacteria; Proteobacteria; alpha
Rhizobiaceae; Sinorhizobium.
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PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
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Lipid degradation;
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29.0%;
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                                                                                                                                             Albright
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Pred. No. 0.04
2; Mismatches
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(VERSION 1).
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01-NOV-1995 (Rel. 32, Las
01-NOV-1995 (Rel. 32, Las
01-NOV-1995 (Rel. 32, Las
HYPOTHETICAL 25.6 KD PRO
Bacteriophage L2.
Viruses; dsDNA viruses, r
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EMBL; M24926; AAA26349.1; -.
PRINTS; PRO0045; EMBL; PRO0045; SIGMA54PCT.
PROSITE; PS00717; SIGMA54_1; 1.
PROSITE; PS00718; SIGMA54_2; 1.
--PROSITE; PS50044; SIGMA54_3; 1.
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           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 94215869.
Maniloff J. Kampo G.J., Dascher C.C.;
"Sequence analysis of a unique temperature phage: mycoplasma virus
                                                                                                                                                                                                                                                                          P42546;
01-NOV-1995
                                                                                Gene 141:1-8(1994).
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nes 27; Conserv
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- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 GVAYSAVVDVIRAAAHEG---VYIEPEARGRLDALREWIYYNYYTERSKRRDRRRRSVCH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: THIS SIGMA FACTOR IS RESPONSIBLE FOR THE EXPRESSION OF THE NITROGEN FIXATION PROTEINS (NIF OPERON), GLNA AND DCTA FOR DICARBOXYLATE TRANSPORT. THE OPEN COMPLEX (SIGMA-54 AND CORE RNA POLYMERASE) SERVED AS THE RECEPTOR FOR RECEIPT OF THE MELTING SIGNAL FROM THE REMOTELY BOUND ACTIVATOR PROTEINS NIFA, NITRC, OR DCTD FOR THE EXPRESSION OF THE REGULATED PROTEINS.

SIMILARITY: BELONGS TO THE SIGMA-54 FACTOR FAMILY.
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32, Last annotation update)
KD PROTEIN (ORF11)
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Pred. No. 4
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AKAAGF -> PRPRDSERCRQAASA (IN
C291DAE1D2DD034C CRC64;
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LEUCINE-ZIPPER (POTENTIAL).
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070695;
15-DEC-1998
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L13696; AAA87967.1; -.
Hypothetical protein.
SEQUENCE 218 AA; 25564 MW
                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         EMBL; U94887; AAC40586.1; -.
Transferase; Nucleotidyltransferase; RNA-directed
SEQUENCE 1305 AA; 150293 MW; 321E9E7F3CF6F11A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 98202706.
Vreede F.T., Huismans H.;
"Sequence analysis of the RNA polymerase gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               African horse sickness virus 9 (AHSV-9) (African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA-DIRECTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sickness virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsRNA viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Arch. Virol. 143:413-419(1998).
-!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (serotype 9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 SQNECVGWLGVAYSAVVDVIRAAAHEG----VYIEPEARGR-----LDALREWIYYNYY 63
                                                                                                                                                        49 GRLDALREWIYYNYYTERSKRRDRRRRSVCHART--WFCFRKYD-----YVRRSI 96
                                                                                                   97
                                                                           80
                                                                                                                               22 GRIDGTK--MYYEYYRYSSKMRETRRKKGTKYKTDDEFLERERDAGRLKLYDLQVIREAS 79
                                                                                                                                                                                                   Local
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                                                                           WED
                                                                                                                                                                                                                                                                                                                                                                                                                           RNA(N).
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l Similarity 24.3%;
17; Conservative :
                                                                                                                                                                                     l Similarity
19; Conserv
                                                                                                     99
                                                                           82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
D RNA POLYMERASE (EC 2.7.7.48) (VP1).
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25564 MW;
                                                                                                                                                                                                   10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reoviridae; Orbivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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Pred. No. 2.2;
L2; Mismatches
                                                                                                                                                                                     Score, 66; DB
Pred. No. 20;
9; Mismatches
                                                                                                                                                                                      9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  African horse
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CRC64;
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STANDARD;

PRT;

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RESULT 8
KF1A_HUMAN
ID KF1A_HUMAN
AC Q12756;
                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                       Matches
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 "use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Karasawa K., Kuge O., Kawasaki K., Nishijima M., Nakano Y., Tomita M., Yokoyana K., Setaka M., Nojima S.;
"Cloning, expression and characterization of plasma platelet-activating factor-acetylhydrolase from guinea pig.";
J. Blochem. 120:838-844(1996).
1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
BY HYDROLYZING THE SN-2 ESTEN BOND TO YIELD THE BIOLOGICALLY
INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
RESIDUE AT THE THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-
                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                        EMBL; D67037; BAA11054.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
15-FEB-2000 (Rel. 39, Last annotation update)
PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
(PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Hystricognathi; Cavildae; Cavia.
                                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P70683;
01-NOV-1997
                                                                  223
                                                                                                             163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                      74 RRSVC-HARTW 83
                                                                                                                            22 LGVAYSAVVDVIRAAHE-----GVYIEPEARGRLDALREWIYY---NYYTERSKRRDRR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                  RGEECSQALSW
                                                                                                          IGIELASHGFIVAAVEHRDESAAATYYFQDAPAAESGNRSWIYYKVGNLETEERKRQLRQ 222
                                                                                                                                                         20;
                                                                                                                                                                  Similarity
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294
349
76
                                                                                                                                                       Conservative
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           STANDARD;
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                                                                                                                                                                                                                                                                                                                   degradation;
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                                                                                                                                                                                                                                                                                               436
                                                                                                                                                                                                            49062 MW;
                                                                                                                                                               10.5%;
                                                                                                                                                                                                                                                                                    SER; 1.

Clycoprotein; Signal.

BY SIMILARITY.

PLATEMET-ACTIVATING FACTOR
                                                                                                                                                      10;
                                                                                                                                                     Pred. No. 6.8;
); Mismatches
                                                                                                                                                              Score 65.5; D. Pred. No. 6.8;
                                                                                                                                                                                                          POTENTIAL. C359D96E392FFE11 CRC64;
                                                                                                                                                                                                                                                   ACETYLHYDROLASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
            PRT;
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4 Phys. 1 (18)

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Query Match
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SEQUENCE
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DOMAIN
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb
or send an email to license@isb-sib.ch).
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-!- FUNCTION: MOTOR FOR ANTERCOGRADE AXONAL TRANSPORT OF SYNAP
                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS50006; FHA_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X90840; CAA62346.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VESICLE PRECURSORS (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE KINESIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
KINESIN-LIKE PROTEIN KIFIA (AXONAL TRANSPORTER OF SYNAPTIC VESICLES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
15-JUL-1998 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIFIA OR ATSV.
                                                                                                                    53 ALREWIYYNYYTERSKRRDRRRRSV----
                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                        7 PAPPV--CDSQNECVGWLGV-----AYSAVVDVIRAAAHEGVYIEPEAR----GRLD 52
FLKEANAISVELKKKVQ 748
                                         ---TTNTISVVSAHSVQ 114
                                                                          ALQKQMDSRYYPEVNEEEEEPEDEVQWTERECELALW-AFRKWKWYQFTSLRDLLWGNAI 731
                                                                                                                                                         PAEPVDWAFAQRELLEKQGIDMKQEMEQRLQELEDQYRREREEATYLLEQQRLDYESKLE 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601255;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00169; PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Microtubules;
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                                                                                                                                                                                                                                          l Similarity
32; Conserv
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429
516
622
801
1575
                                                                                                                                                                                                                                          Conservative
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383
462
572
681
822
1673
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                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                          Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                                           MW.
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MECHANOCHEMICAL (MOTOR).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
D8DDEC784624FB4D CRC64;
                                                                                                                    -CHARTWFCFRKYDY-----VRRSIWHDT- 101
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                                                                                                                                                                                                                                                          DB 1;
43;
                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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                                                                                                                                                                                                                                        56;
                                                                                                                                                                                                                                                                             Length 1690;
                                                                                                                                                                                                                                      Indels,
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                                                                                                                                                                                                                                      Gaps
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KF1A MOUSE
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101-QCT-1993 (Rel. 27, Created)

101-NQY-1997 (Rel. 35, Last sequents of the sequents of th
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KF1A MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as is content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIF1A OR KIF1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY SEQUENCE OF 100-247 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 95292344.
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                                                                                                                                                                                                                                                                                                                                           MGD; MGI:108391; KIFIA.

PRINTS; PR00380; KINESINHEAVY.

PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1;

PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2;

PROSITE; PS50003; PH_DOMAIN; 1.

PROSITE; PS50006; FHA_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Kinesin family in murine central nervous system.";
J. Cell Biol. 119:1287-1296(1992).
-1- FUNCTION: MOTOR FOR ANTEROGRADE AXONAL TRANSPORT OF SYNAPTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                   DOMAIN
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SIMILARITY: BELONGS TO THE KINESIN-LIKE
SUBFAMILY.
SIMILARITY: CONTAINS 1 FHA DOMAIN.
SIMILARITY: CONTAINS 1 PH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VESICLE PRECURSORS.
SUBUNIT: MONOMER.
SUBUNIT: MONOMER.
TISSUE SPECIFICITY: EXPRESSED ALMOST EXCLUSIVELY IN ADULT BRAIL
TISSUE (MAINLY IN THE CEREBELLUM AND CEREBRUM) WITHIN A SINGLE
TYPE OF NEURONAL CELL. WITHIN THE NEURONAL CELL LEVELS ARE
CONCENTRATED AROUND THE AXON, WITH SMALLER AMOUNTS IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81:769-780(1995)
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                                               Microtubules;
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FHA; 1.
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36, Last annotation update)
EIN KIF1A.
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     191724
                                                                              ; ATP-binding; Coiled coil.
MECHANCCHEMICAL (MOTOR).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
FHA.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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     (BY SIMILARITY).
D6EC3B88CBC9CCC6 CRC64;
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Best Local Similarity
Matches 32; Conser
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Q61885; Q62003;
Q1-NOV-1997 (Rel
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Modentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                       Amiguet P., Gardinier M.V., Zanetta J.-P., Matthieu "Purification and partial structural and functional of mouse myelin/oligodendrocyte glycoprotein.";
J. Neurochem. 58:1676-1688(1992).
-I- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH.
                                                                                                                                                                                                                                                                                                                                                                    Pham-Dinh D., Mattei M.-G., Nussbaum J.-L., Roussel G.
Pontarotti P., Roeckel N., Mather I.H., Artzt K., Lind
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 29-246 FROM N.A. STRAIN-BALB/C; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gardinier M.V., Matthieu J.M.;
"Murine and human MOG are highly conserved: cDNA analysis.";
Trans. Am. Soc. Neurochem. 24:234-234(1993).
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                                                                                                                                                                                                                      STRAIN-BALB/C; TISSUE-BRAIN;
MEDLINE; 92218912.
Amiguet P., Gardinier M.V.,
                                                                                                                                                                                                                                                                                              "Myelin/oligodendrocyte glycoprotein is a member of a immunoglobulin superfamily encoded within the major histocompatibility complex."; proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 93376728.
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"Structure and polymorphism
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                                                                                                                                                                                                                                                                                                                                                        Dautigny A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycoprotein gene.
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              DISEASE: REDUCED CONCENTRATIONS OF MOG ARE OBSERVED IN QUACKING DYSMYELINATING MUTANT MICE.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                    SUBUNIT: MAY FORM HOMODIMERS,
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TIASUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE
LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE C
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                                                                                                                                 CELL COMMUNICATION
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                                                         MEMBRANES
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Pred. No.
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ANCE OF THE MYELIN SHEATH AND
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characterization
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                                                JIMPY AND
                                                                           CYTOPLASMIC
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V-LIKE DOMAIN.

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SUPERFAMILY. CONTAINS SUBFAMILY.

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Query Match
Best Local S
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DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                                                                                                          Seeger K.J., Harris D., Parkhill J., Barrell B.G., I Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databa-i- CATALYTIC ACTIVITY: LL-2,6-DIAMINOHEPTANEDIOATE
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DISULFID
CARBOHYD
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                                                                                                                  -1- PATHWAY: SIXTH STEP
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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    SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
    SIMILARITY: BELONGS TO THE DIAMINOPINELATE EPIMERASE FAMILY.

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                                                                                                  SEMIALDEHYDE.
                                                                                                                                         DIAMINOHEPTANEDIOATE.
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       SWISS-PROT entry is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
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37.5%;
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copyright. It is produced through a collaboration
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R -> G (IN REF. 4).

B -> E (IN REF. 3).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthesis."
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3B998569F8A96449 CRC64;

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                                                                                                                                                                    EMBL; D50840; BAA09451.1;
                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 93:4638-4643(1996).
-!- FUNCTION: MAY SERVE AS "FLIPPASE" AS WELL AS A GLUCOSYLTRANSFERASE
THAT TRANSFERS GLUCOSE TO CERAMIDE.
-!- CATALYTIC ACTIVITY: UDD-GLUCOSE + N-ACYLSPHINGOSINE =
UDP + D-GLUCOSYL-N-ACYLSPHINGOSINE.
-!- PATHWAY: FIRST GLYCOSYLATION STEP OF GLYCOSPHINGOLIPID SYNTHESIS.
-!- SUBCELLULAR LOCATION: TYPE III MEMBRANE PROTEIN. ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
CERAMIDE GLUCOSYLTRANSFERASE (EC 2.4.1.80) (GLUCOSYLCERAMIDE SYNTHASE)
(UDD-GLUCOSE:N-ACYLSPHINGOSINE D-GLUCOSYLTRANSFERASE) (GLCT-1)
                                                                                                                                                                                                                                                                                                                                                                                                               -!- TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FRAGMENI).
Homo sapiens (Human).
Homo sapiens (Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01326; DAP_EPIMERASE; 1. ISOMERASE; Lysine biosynthesis. ACT_SITE 85 85 BY SIM ACT_SITE 218 218 BY SIM SEQUENCE 289 AA; 30014 MW; 3F84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ichikawa S., Sakiyama H., Suzuki G., Hidari K.I., Hirabayashi Y.;
"Expression cloning of a cDNA for human ceramide glucosyltransferase
that catalyzes the first glycosylation step of glycosphingolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 ALPAPP-----VCDSQNECVGWLGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREW
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                                                                                                                      reticulum
                                                                                                                                        Glycosyltransferase; Transmembrane;
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Pred. No.
                    (POTENTIAL).
POTENTIAL.
                                                                     SIGNAL-ANCHOR
                                                                                            LUMENAL (POTENTIAL)
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BY SIMILARITY.
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                                                                (TYPE-IB MEMBRANE PROTEIN)
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                                                                                                                                        Signal-anchor;
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Best Local
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Best Local S
Matches 11
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"Plant 2107 protein, a nuclear antigen associated with cell division as component of the 26S proteasome.";

Elant Physiol. 113:281-291(1997).

"Elant Physiol. 113:281-291(1997).

"Elant Protection: MAX PLAY A ROLE IN REGULATION OF THE 26S PROTEASOME CACTIVITY OR SPECIFICITY IN RELATION TO CELL PROLIFERATION.

"El-1-SUBCELLULAR LOCATION: NUCLEAR.

"El-1-SUBCELLULAR LOCATION: TO THE PROTEASOME SUBUNIT S3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSD3_DAUCA
Q06364;
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
MEDLINE; 97161126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith M.W., Ito M., Yamada T., Suzuki T., Komamine A., "Isolation and characterization of a cDNA clone for plant nuclear antigen 21D7 associated with cell division.", plant Physiol. 101:809-817(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith M.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 94143479.
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                                                                                                                                                                                                                                                                              EMBL; D13434; BAA02696.1; -. PFAM; PF01399; PCI; 1.
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el. 37, Last annotation update)
REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7).
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55351 MW;
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                                                                                           .18;
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Pred. No.
                                                                 Score 63; DB Pred. No. 15; 6; Mismatches
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MICROTUBULE-BINDING (POTENTIAL).
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P36022;
01-JUN-1994
01-JUN-1994
15-FEB-2000
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Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DYHC_YEAST
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                                                                                                                                                                                                                        EMBL; Z21877; CAA79923.1;
EMBL; L15626; AAA16055.1;
EMBL; Z28279; CAA82132.1;
PIR; S38128; S38128.
                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way useful.
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"Disruption of mitotic spindle orientation in a yeast dynein mutant.";

Proc. Natl. Acad. Sci. U.S.A. 90:10096-10100(1993).

-I- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A MOTOR FOR THE INTRACELULIAR RETROGRADE MOTILITY OF VESICLES AND ORGANIZLES ALONG MICROTUBULES. REQUIRED TO MAINTAIN UNIFORM NUCLEAR DISTRIBUTION IN HYPHAE. MAY PLAY AN IMPORTANT ROLE IN THE PROPER ORIENTATION OF THE MITOTIC SPINDLE INTO THE BUDDING DAMIGHTER OFFIT. VERSON
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L1 Y.-Y., Yeh E.Y.,
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Motor protein; Microtubules;
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SUBCELLULAR LOCATION: CYTOPLASMIC. PROBABLY
THE INNER PLASMA MEMBRANE.
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SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND
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-i- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED J. COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
                                                                                                                                                                                                                                                                                                                                                                                        Wyelin/oligodendrocyte glycoprotein is a member of a subset of immunoglobulin superfamily encoded within the major inistocompatibility complex.";
Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pham-Dinh D., Mattei M.-G., Nussbaum J.-L., Roussel G., Pontarotti P., Roeckel N., Mather I.H., Artzt K., Lindahl K.F.,
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wyelin/oligodendrocyte glycoprotei
immunoglobulin superfamily.";
J. Neurosci. Res. 33:177-187(1992).
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ACTIVE MYELINATION.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.

CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)

WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).
                                                                                                                                                            CELL COMMUNICATION.
SUBUNIT: MAY FORM HOMODIMERS.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT
                                                                                          DEVELOPMENTAL STAGE: A PEAK OF EXPRESSION HAS BEEN OBSERVED BETWEEN POSTNATAL DAYS 15 AND 25, COINCIDENT WITH THE PERIO
                                                                                                                                    LOCALIZED ON THE SURFACE OF MYELIN AND OLICODENDROCYTE CYTOPLASMIC MEMBRANES.
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Pred. No. 1.5e+02;
3; Mismatches 33;
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EMBL; L21995; -; NOT_ANNO
PFAM; PF00047; ig; 1.
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                                                                                CYTOPLASMIC (POTENTIAL).
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                                                                                                                           MYELIN-OLIGODENDROCYTE GLYCOPROTEIN
                                                                                                                                                   Signal
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뮍 Ş Matches 64 19 VGWLGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREWI 58 VGWYRSPFSRVVHLYRNGKDQDAEQAPEYRGRTELLKESI L Similarity 15; Conserv Conservative υ •• Mismatches 20; 103 Indels 0,

Query Match Best Local

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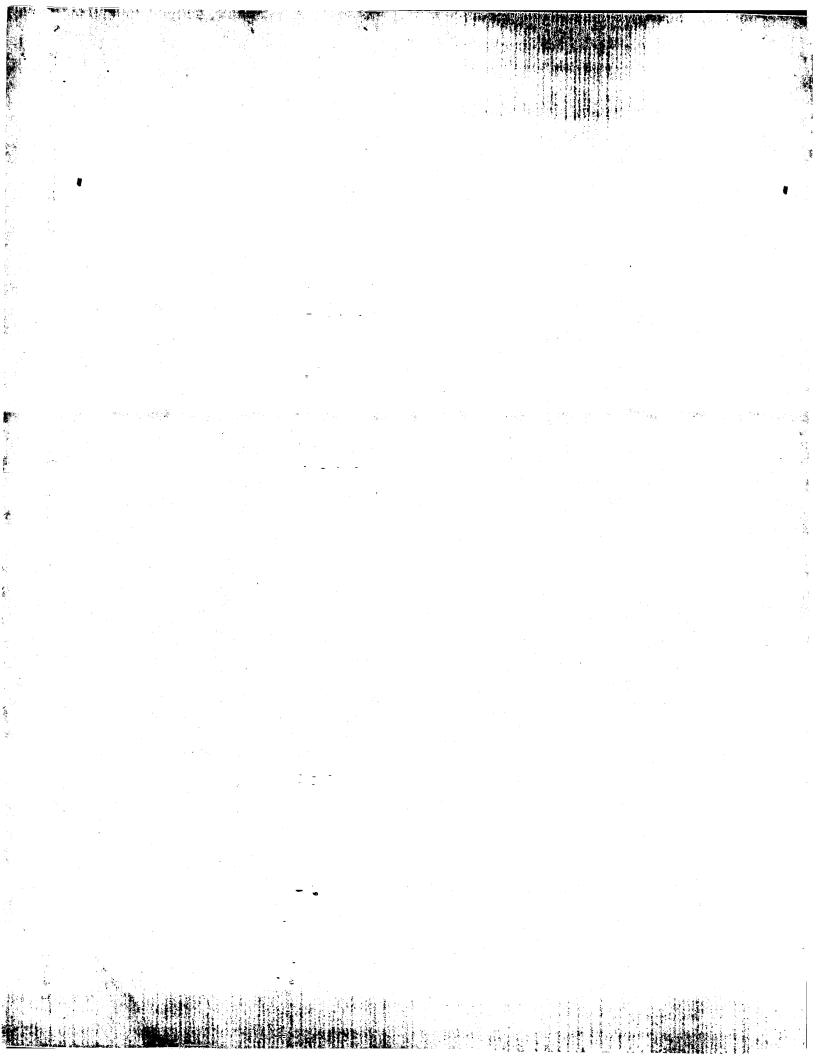
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Search completed: June 23, Job time: 672 sec 2000, 10:14:51



GenCore version Copyright (c) 1993 - 2000

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Q92vk3 arabidopsis
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Q64304 rattus louc
Q53718 mycobacteri
Q9298 arabidopsis
Q9359 brachydanio
Q48839 arabidopsis
Q19843 caenorhabdi
Q9370 brachydanio
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Q64866;
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JAVIER R., SHENK T.;

"Mammary tumors induced by human adenovirus type

"trail early region 4 gene.";

Breast Cancer Res. Treat. 39:57-67(1996).

EMBL; S82508; AAB37507.1;

EMBL; S82508; AAB37507.1;

EE2C2416 CRC32;
01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-NOV-1998 (TIEMBLIEL 08, Last annotation update)
ADENOVIRUS TYPE 40, COMPLETE GENOME.
Human adenovirus type 40.
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(TremBirel. 08, Last annotation update)
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KIDD A.H., ERASMUS M.J.;

"Sequence characterization of the Virology 172:134-144(1989).
                                                                             PIENIAZEK N.J., SLEMENDA S.B., PIENIAZEK D., I
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ
EMBL; L19443; AAC13982.1; -.
SEQUENCE 121 AA; 13976 MW; 8B84054F CRC32;
                                                                                                                                                                                                                                                                                                   MEDLINE; 90111698.

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"The adenovirus type 40 hexon: sequence, predicted relationship to other adenovirus hexons.";

J. Gen. Virol. 70:3203-3214(1989).
                                                                                                                                                                                                                  MEDLINE; 94087748.

DAVISON A.J., TELFORD
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                                                                                                                                                               SEQUENCE FROM N.A.
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to that of adenovirus type 5.";
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Submitted (APR-1995) to the
EMBL; U24436; AAA66077.1; -
PFAM; PF01359; Transposase_
SEQUENCE 347 AA; 40758 M
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MEDLINE; 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A. KERLAYAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D. OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J. SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J. THUREMANN J. F. GEOGHAGEN N.S.M., PETERSON J.D., SADOW P.W. THERE A.D., SADOW P.W.
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Q58318;
                                                                                                      UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C., COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M., KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C., "COmplete genome sequence of the methanogenic archaeon, Methanococcus and the complete genome sequence of the methanogenic archaeon, Methanococcus and the complete genome sequence of the methanogenic archaeon, Methanococcus and the complete genome sequence of the methanogenic archaeon, Methanococcus and the complete genome sequence of the methanogenic archaeon, Methanococcus and the complete genome sequence of the methanogenic archaeon, Methanococcus and the complete genome sequence of the methanogenic archaeon, Methanococcus and the complete genome sequence of the methanogenic archaeon and the complete genome sequence of the methanogenic archaeon.
                         Science 273:1058-1073(1996).
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Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Sciaroidea;
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Mayetiola destructor (Hessian fly).
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26; Conserv
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AA; 40758 MW;
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l6; Mismatches
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MERRICK J.M., GLODEK A.,
FUHRMANN J.L., NGUYEN D.
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                   AND M. JANNASCHII
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                                                                                                                                                                                                                                                                                                                          J.D.,
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TIGR; MJ0908; ·
Hypothetical pi
SEQUENCE 123:
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ROUNSLEY S.D., LIN X., KAUL S., SHEA T.P., FUJII C.Y., MASON T.M.
SHEN M., RONNING C.M., FRASER C.M., SOMERVILLE C.R., VENTER J.C.
"Arabidopsis thaliana chromosome II BAC 75B13 genomic sequence."
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AC005398; AAC65978.1:
SEQUENCE 945 AA; 108084 MW; 88791777 CRC32:
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eudicotyledons; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
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Viruses; dsDNA viruses, orthopoxvirus.
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                                                                               Poxviridae; Chordopoxvirinae;
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Best Local Similarity
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Q64304;
Q1-NOV-1996
Q1-NOV-1998
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PROTEIN LINKED TO SYSTEM L-LIKE NEUTRAL AMINO ACID ACTIVITY.
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                                                                                                                                               neutral a (CD98).";
                                                                                                                                                                                                                  STRAIN-SPLAGUE-DAWLEY; TISSUE-LIVER; MEDLINE; 98395066.
KANAI Y., SEGAWA H., MIYAMOTO K., UC
                                                                                                                                                                                                                                                                                                                                   STRAIN-SPRAGUE DAWLEY: TISSUE-JEJUNAL BRUSH BORDER; YAO S.Y.M., MUZYKA W.R., CHEESEMAN C.I., ELLIOTT J. Submitted (MAY-1996) to the EMBL/GenBank/DDBJ datab
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96128073.

BRODER S., BRODER A., HAMPRECHT B.;

BRODER S. BRODER A., HAMPRECHT B.;

The 4F2hc surface antigen is necessary for expression of like neutral amino acid-transport activity in C6-BU-1 rat cells: evidence from expression studies in Xenopus laevis Biochem. J. 312:863-870(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus leucopus (mottle-tailed rat), and Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
                                   EMBL; X89225; CAA61509.
EMBL; U59324; AAC53560.
EMBL; AB015433; BAA3303
PFAM; PF00128; alpha-an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                         KANAI Y., SEGAWA H., MIYAMOTO K., UCHINO H.,
Expression cloning and characterization of a
neutral amino acids activated by the heavy of
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 VYHDTNYN 268
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                                                                                                                                 Biol.
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                                                                                                                                                                       amino acids
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                                                                                                      CAA61509.1;
                alpha-amylase;
AA; 58072 MW;
                                                                                                                              273:23629-23632(1998).
                                                              BAA33036.1;
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65281 MW;
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Sciurognathi; Muridae; Murinae;
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Pred.
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1.
6C2869F1 CRC32;
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                                                                                                                                                                                                                                                                                                                                          databases
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CHERNOS V.
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Best Local S
Matches 17
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Best Local S
Matches 18
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2003718

PRELIMINARY; PRT; 284 AA.

2003718

O1-UNN-1998 (TremBirel. 06, Created)

O1-NOV-1998 (TremBirel. 06, Last sequence update)

O1-NOV-1998 (TremBirel. 08, Last annotation update)

HYPOTHETICAL 31.8 KD PROTEIN.

MTV036.18C.
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                                                                                         Q9ZQ98 PRELIMINARY; PKT; 490 AA.
Q9ZQ98;
Q1-MAY-1999 (TIEMBLIFEL 10, Created)
O1-MAY-1999 (TIEMBLIFEL 10, Last sequence update)
O1-NOV-1999 (TIEMBLIFEL 12, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Eukkryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
                                                                         PUTATIVE GLUCOSYL TRANSFERASE F13K3.16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 284 AA; 31801 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
EMBL; AL021931; CAA17389.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K.,
BALASUBRAMANIAN V., HEYM B., BERGH S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Myco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLE S.T., PARKHILL J., Submitted (FEB-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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ilarity 29.5%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                     Score 64.5; D
Pred. No. 16;
9; Mismatches
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Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7A6BB7C1 CRC32;
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BLOOM B.R., JACOBS
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                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                                                                                                          21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 284;
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                                                                                                                                                                                                                                                                                                                                                                       9;
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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  RESULT 11
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ID O48839
AC O48839
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Best Local (
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Best Local s
Matches 20
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  048839
048839;
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01-NOV-1998
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                                                                                                                         189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tansferase
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                    PRELIMINARY;
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SEQUENCE FROM N.A.

OATES A.C.;
Thesis (1998), University of Melbourne,
EMBL; AJ005590; CAA06674.1; -
HSSP; P80631; 2HCK.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygil; Teleostei; Euteleostei; Ostariophysi; C
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                        PFAM; PF00069; pkinase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIN X., KAUL S., SHEA T.P., FUJII C.Y., SHEN M., VANAKEN S.E.,
BARNSTEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENITO M.,
CARRERA A.J., CREASY T.H., BUELL C.R., TOWN C.D., NIERMAN W.C.,
FRASER C.M., VENTER J.C.;
"Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence.",
submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006282; AAD20152.1; -.
EMBL; PS00375; UDPGT; 1.
                                                                                                                                                                                                                                                    Praisferase.
Promence 1095 AA; 125171 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             core eudicots;
Arabidopsis.
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                                         65 ERSKRRDRRRRSVCHARTWFCFRKY 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275 QDECIKWLDSKDVESVLYVCLGSICNLPLAQLRELGLGLEATKRPFIWVIRGGGKYHELA 334
                                                                                                                    5 ALPAPPVCDSQNECVGWLGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREWIYYNYYT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 QNECVGWLG------VAYSAVVDVIRAAAHE-GVYIEPEAR-----GRLDALR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 EWIYYNYYTERSKRR 70
KNMREHIQNQHLVTRKRIRFRFRRF 213
                                                                                 AVSVPVSLEFQEECLG-----LAVLDIMRLAKEKG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EWILESGFEERTKER 349
                                                                                                                                                                  l Similarity
19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TremBirel 08, Created)
(TremBirel 08, Last sequence update)
(TremBirel 12, Last annotation updat
OSINE KINASE (EC 2.7.1.112).
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                                                                                                                                                                Conservative 17;
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                                                                                                                                                                                 10.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                   Score 64.5;
Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 64.5;
Pred. No. 31;
                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                961AB4C1 CRC32;
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                                                                                                                                                              36;
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                                                                               KSPVDIYNHSSYKSFLP 188
                                                                                                                                                                Indels
                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinopterygii;
                                                                                                                                                                                                      1095;
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                                                                                                                                                              13;
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                                                                                                                                                            Gaps
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                               THIERRY-MIEG J.,
                                                                                                                                                                                                                                                     WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCHURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN PARSONS J., PERCY C., RIFKEN L., ROOPRA R., SULSTON J.,
SMALDON N., SMITH A., SONNHAMMER E., STADER R., SULSTON J.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WANTSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q19843;
Q19843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease.
SEQUENCE
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ROUNSLEY S.D., LIN., KETCHUM K.A., CROSBY M.L., BRANDO
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS N
SOMERVILLE C.R., VENTER J.C.;
SUMBILTED (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC003974; AAC04485.1; -.
PFAM; PF00442; UCH-1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
WATERSTON
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 94150718. WILSON R., AINSCOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-NOV-1998 (TIEMBLIEL. 08, Last annotation update)
SIMILARITY TO HUMAN FOLICULAR VARIANT TRANSLOCATION
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01-JUN-1998 (TIEMBLIFEL 06,
01-MAX-1999 (TIEMBLIFEL 10,
PUTATIVE UBIQUITIN SPECIFIC
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                                                 SEQUENCE FROM N.A.
                                                                                                     Submitted (FEB-1996)
                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                SEQUENCE FROM N.A. BENTLEY D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 SQNECVGWLGVAYSAVVDVIRAAAHEGVYI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDNECENWEDLAVDSEEVIVKRDARKKVLINKAPPVLTIHLKRFSQDARGRVSKLSGHVD 990
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(FEB-1996)
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Last sequence update)
Last annotation updat
PROTEASE.
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Pred. No. 88;
L2; Mismatches
EMBL/GenBank/DDBJ databases
                                                                                                  EMBL/GenBank/DDBJ databases
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RESULT
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Best Local (
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                                                                                                                                               094512
094512;
01-MAY-1999
01-MAY-1999
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01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00
Paired box;
SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           093370
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PROBABLE INVOLVEMENT IN ERGOSTEROL BIOSYNTHESIS SPBC646.08C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Development 125:3063-3074(1998).
-!- SUBCELLULAR LOCATION: NUCLEAR
-!- SIMILARITY: CONTAINS A PAIRED
EMBL; AF072547; AAC31811.1; -.
HSSP; P06601; 1PDN.
PROSITE; PS00034; PAIRED_BOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U49829; AAA93385.1; -. SEQUENCE 264 AA; 29808 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFEFFER P.L., GERSTER T., LUN K., BRAND M., BUSSLINGER M.; "Characterization of three novel members of the zebrafish Pax2/5/8 family: dependency of Pax5 and Pax8 expression on the Pax2.1 (noi)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; C
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00292; PAX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 98337826.
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box; DNA-binding; Developmental protein;
E 386 AA; 41541 MW; 5BCDF72B CRC32;
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                                                                                                                  (TIEMBLIEL. 10, Created)
(TIEMBLIEL. 10, Last sequence update)
(TIEMBLIEL. 10, Last annotation updat
VOLVEMENT IN ERGOSTEROL BIOSYNTHESIS.
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                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Pred. No. 19;
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Pred. No. 30;
                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                       update)
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                                                                       Query Match 10.2%;
Best Local Similarity 34.1%;
Matches 14; Conservative
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
SOURCE S.D., TSCHUDY, M.M., LIN X., KETCHUM K.A., CROSBY M.L.,
RONNSLEY S.D., TSCHUDY, M.M., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
BRANDON R.C., SPRIGGS T.A., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMERVILLE C.R., VENTER J.C.;
SUMMITTED C.R., VENTER J.C.;
SUMMITTED C.R., VENTER J.C.;
SUMMITTED C.R., VENTER J.C.;
SUMMITTED C.R., VENTER J.C.;
SEQUENCE 756 AA; 85182 MW; F71F6CF4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                              022863;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL PROTEIN.
T01024.23
                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viriddiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
euphyllophytes; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              022863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEEGER K., HARRIS D., WOOD V., RAJANDREAM M.A., BARRELL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AL035216; CAA22812.; -
SEQUENCE 516 AA; 58692 MW; BA471658 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
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355 WLWILHRIVVDVVRIDSHLEFYEDPGNLGRMSDILAVYAWV 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 KRR--DRRRRSVCHARTWFCFRKYDYVRRSIWHDTTTNTISVVSAHSVQ 114
                                  21 WLGVAYSAVVDVIRAAHEGVYIEPEARGRLD---ALREWI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 WIGVAYSAV-------VDVIRAAAHEGVYIEPEARGRIDALREWIYYNYYTERS 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.2%; Score 63.5; DB 22.9%; Pred. No. 42; Live 14; Mismatches
                                                                     Score 63.5; DB 10; Length 756; Pred. No. 66; 7; Mismatches 17; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            756 AA.
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Run on:
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Maximum DB seq length: 1000000
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Perfect score:
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed;
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
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/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
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US-08-630-820-5
US-08-723-624-19
US-08-818-772A-2
US-08-818-772A-2
US-08-819-866-1
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US-08-819-868-2
US-08-91-248-2
US-08-453-921-4
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US-08-453-921-2
US-08-453-921-3
US-08-304-309-3
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US-08-391-342-3
US-08-391-342-3
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Sequence 26, Appl
Sequence 28, Appl
Patent No. 5432081
Sequence 14, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 6, Appli
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09-4/c 4, Application US/08735609 1NFORMATION: ANT: Chamberlain, Jeffrey ANT: Chamberlain, Jeffrey ANT: Amalitano, Andrea ANT: Hauser, Michael A. ANT: Hartigan-O'Connor, D OF SEQUENCES: 15 PONNENCE ADDRESS: ESSEE: Medlen & Carroll, ESSEE: California E California UNITYE: Floppy disk UTTRY: United States Of Ame 94104 ER READABLE FORM: UTTPE: Floppy disk UTTRY: IBM PC Compatible UTTRY: UNITED FORMATION TYPE: Patentin Release #1 TAPPLICATION NUMBER: US/08/735 NG DATE: INGOLIA, Diane E. SIFICATION NUMBER: US/08/735 EEV/AGENT INFORMATION: INGOLIA, Diane E. SIFICATION INFORMATION: MMUNICATION INFORMATION: MMUNICATION INFORMATION: 11 INFORMATION: 1415) 397-8338 ETAN: (415) 397-8338 ETAN: (415) 397-8338 ETAN: (415) 397-8338 ETAN: TYPE: Other nucleic acid NNDEDNESS: double NNDEDNESS: double NNDEDNESS: other nucleic acid NDEDNESS: other nucleic acid SELETYPE: Other nucleic acid		77777777777777777777777777777777777777
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Query Match Best Local Similarity Matches 345; Conserv

Conservative

100.0%; Score 345; DB 4; 100.0%; Pred. No. 2.3e-112; Mismatches 0;

Length 34303; Indels

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; MOLECULE TYPE: US-08-374-483-6
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Best Local S
Matches 345
                                                                                                                                                                                      TELEFAX: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 34382 bass Type.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                     Local Similarity
les 345; Conserv
                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: 111
                                                                                                                                                                                  LENGTH: 34382 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 17-JAN CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLE OF INVENTION:
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 1 atggttcttccagctcttcccgctcctcccgtgtgtgtgactcgcagaacgaatgtgtaggt 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEORGE, SAMUEL E.
                                                                                                                                                         linear
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                                                                                                                                  DNA (genomic)
                                                                                                                                                                   single
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                                    100.0%; Score 345; DB 3;
100.0%; Pred. No. 2.3e-112;
Live 0; Mismatches 0;
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Query Match
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Matches 345; Conserv
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                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ. ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5955360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMAPPLICANT:
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                MOLECULE TYPE:
DESCRIPTION:
                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pai
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/735,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE Medlen & Carroll, LLP
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chamberlain, Jeffrey S. APPLICANT: Amalfitano, Andrea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 acgaccaacacgatctcggttgtctcggcgcactccgtacagtag 345
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                                                            TOPOLOGY:
                                                                              STRANDEDNESS:
                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
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                                                            linear
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                /desc = "DNA"
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100.0%; Score 345; DB 4; 100.0%; Pred. No. 2.3e-112; tive 0; Mismatches 0;

Length 35935; Indels

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                                                                                                                                                         APPLICATION NUMBER: WO PCT/FR94/00624
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 06482
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         equence 43, Application_US/08379452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34162 AACTACTACACAGAGCGATCTAAGCGGCGAGACCGGAGACGCAGATCTGTTTGTCACGCC 34103
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                                                                                   REFERENCE/DOCKET NUMBER: 0
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34042 ACGACCAACACGATCTCGGTTGTCTCGGCGCACTCCGTACAGTAG 33998
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                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: DS-
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: IMLER, Jean-Luc
PPLICANT: MEHTALI, Majid
PPLICANT: PAVIRANI, Andrea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Virginia
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/OFFILING DATE: 26-JAN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States ZIP: 22314-2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TILE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING TILE OF INVENTION: COMPLEMENTATION LINES
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aactactacacagagcgatctaagcggcgagaccggagacgcagatctgtttgtcacgcc 240
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; Sequence 2, Application US/08462014
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Best Local Similarity 100.0%;
Matches 345; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34342 ATGGTTCTTCCAGCTCTTCCCGCTCCCCCGTGTGTGACTCGCAGAACGAATGTGTAGGT 34283
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                                                                         TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 8299 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34162 AACTACTACACAGAGCGATCTAAGCGGCGAGACCGGAGACGCAGATCTGTTTGTCACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                             REFERENCE/DOCKET NUMBER: UP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gao, Guang-Ping
IIILE OF INVENTION: Method for Improved Production of
IIILE OF INVENTION: Recombinant Adeno-Associated Viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/O FILING DATE: 05-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                   TOPOLOGY:
                                      STRANDEDNESS:
                                                          TYPE: nucleic acid
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PA
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Spring House Corporate Cntr., P.O. Box 457
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                     unknown
                                           double
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Pred. No. 2.3e-112;
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33283 AGTTGGATGACTGAGCGGCAGCAGCGAAAGGACGGCCGCAGGAGGGGTATATGCTGTTCA 33224

181 aactactacacagagcgatctaagcggcgagaccggagacgcagatctgtttgtcacgcc 240

33343 TTTTTTATTTCATCAGATGCAGAGGAACTTCTCCAGAATCTTCGAGAATGGATGTACTTC 33284

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Best Local Similarity
                                                                                                                                                                                    Matches 145; Conservative
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                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 35081 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Seide, Rochelle K
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: A313
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,705-5000
                                                                                                                 33460 ATGGTTCTTCCAATCCTGCCACCGCCCCCTCTGAATGATAGAC---AAGGCAGCATTAAC 33404
                                                        33403
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APPLICATION NUMBER: US
FILING DATE: 20-NOV-19
121 gtttacatagaacccgaagccagggggcgcctggatgctttgagagagtggatatactac 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P.
STREET: 30 Rockefeller Plaza
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
TIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                            1 atggttettecagetettecegetecteeegtgtgtgaetegeagaacgaatgtgtaggt 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LE OF INVENTION
                                                tggctgggtgtggcttattctgcggtggtggatgttatcagggcagcggcgcgcatgaagga 120
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Smith, Alan E.
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20-NOV-1996
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                                                                                                                                                                              Score 54; DB 3; Length 35081;
Pred. No. 7e-09;
0; Mismatches 130; Indels
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Pred. No. 1.8e-18;
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                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (317) 231-74
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                 1071 CGCATGTCGCGCAAGACTGTAACCACGCGTCTGTTGACTGGCAGGTGGTGGCCAATGGTG 1130
1191 GCGGGACTTTGCAAGTGGTGA 1211
                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,267
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2633 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                           83 cggtggtggatgttatcagggcagcggcgcatgaaggagtttacatagaacccgaagcca 142
                                                                                                                                                      23 ctcctcccgtgtgtgactcgcagaacgaatgtgtaggttgggttgtggttgtggttattctg 82
                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT: Ramsay, Nichola TITLE OF INVENTION: Control OMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Breen, John P.
REGISTRATION NUMBER: 38
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                99999cgcctggatgctttga 163
                                                                ATGTCAGCGTTGAACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGCACTA 1190
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11 South Meridian
                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                       Score 29;
Pred. No.
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                       DB 2;
1.3;
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                                                                                                                                                                                                                                       Length 2633;
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Best Local Similarity 50.4%;
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                                                                                                                                                        Patent No. 60080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 3035 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: BTIF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPAX: 512/474-7577
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                                                                                                                                       SENERAL INFORMATION:
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'MEDIOM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC CODS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/723,624
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rose, Alan B. APPLICANT: Last, Robert L
                                                                                                                                                                                                                                                                                 1915 GCGGGACTTTGCAAGTGGTGA 1935
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1795 CGCATGTCGCGCAAGACTGTAACCACGCGTCTGTTGACTGGCAGGTGGTGGCCAATGGTG 1854
                TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TILE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING THE EXPRESSION OF GENES IN PLANTS
                                                                                APPLICANT:
                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                   143 gggggcgcctggatgctttga 163
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SEQUENCES:
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                                                                        BOSSLET, Klaus
CZECH, Joerg
                                                                                                                      Martin
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US-08-723-624-19

Patent No.

GENERAL INFORMATION: APPLICANT: Rose,

Rose, Alan B. Last, Robert L. Sequence 19,

Application US/08723624

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US-08-630-820-5
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Best Local S
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/630,820 FILING DATE: 10-APR-1996 PRIOR APPLICATION DATA: DE 19513676.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Foley & L
                                                               1984 ATGTCAGCGTTGAACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGCACTA 2043
                                                                                                                                   1924 CGCATGTCGCGCAAGACTGTAACCACGCGTCTGTTGACTGGCAGGTGGTGGCCAATGGTG 198
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NAME/KEY:
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LENGTH: 3169 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 11-APR-1995
ATTORNEY/AGENT INFORMATION:
2044 GCGGGACTTTGCAAGTGGTGA 2064
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN: pRAJ210
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                  143
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REFERENCE/DOCKET NUMBER:
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Local Similarity 50.4%;
hes 71; Conservative
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TOPOLOGY: cir
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LOCATION: 3..641
                                                                                             cgqtggtggatgttatcagggcagcggcatgaaggagtttacatagaacccgaagcca 142
                           gggggcgcctggatgctttga 163
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (202)672-5300
(202)672-5399
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666..3162
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Pred. No. 1.5;
0; Mismatches 70; Indels
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US-08-723-624-19
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SEQUENCE CHARACTERISTICS:
LENGTH: 3824 base pair
                                                                                                                                                                                                                                                             tent No. 5801027
                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                      APPLICANT: Ramsay, Nichola TITLE OF INVENTION: Contro NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         2704 GCGGGACTTTGCAAGTGGTGA 2724
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NAME: Parker, David L.

REGISTRATION NUMBER: 32,165
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TELEPHONE: 512/418-3000
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APPLICATION NUMBER: US/08/723,624
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 OPERATING SYSTEM:
                                                             COUNTRY: UZIP: 46204
                                                                                                                           STREET:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                         Indianapolis
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11 South Meridian
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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50.4%;
                                                                                                                                                                                  Control of Genes in Transgenic Plants
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Pred. No. 1.6;
0; Mismatches
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                                                                             COMPUTER: IBM PC/AT
OPERATING SYSTEM: DOS VE
SOFTWARE: WORDERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: 15-MAR-199;
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08318772A
Patent No. 5679558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-318-772A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GOBEL, Elke
APPLICANT: NAKAKIDO, Fumio
TTTTLE OF INVENTION: Transformation of monocot cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1126 ATGTCAGCGTTGAACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGCACTA 1185
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IMMEDIATE SOURCE:
CLONE: PUMIGIT
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
                                                                                                                                                                                                                                                                       STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DN
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CURRENT APPLICATION DATA:
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                                                APPLICATION NUMBER: PCT/EP93/00905
FILING DATE: 14-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 gggggcgcctggatgctttga 163
APPLICATION NUMBER: EP 92401066.3 FILING DATE: 15-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 cggtggtggatgttatcagggcagcggcatgaaggagtttacatagaacccgaagcca 142
                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 ctcctcccgtgtgtgactcgcagaacgaatgtgtaggtttggctggggtgtggcttattctg
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Breen, John P. REGISTRATION NUMBER: 38,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/452,267 FILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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                                                                                                                                                                                     E: Floppy disk
IBM PC/AT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                circular
                                                                                                    15-MAR-1995
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                                                                                                                                                                      DOS version 3.3
                                                                                                                    US/08/318,772P
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Gaps 82

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5642 base pairs
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Jeffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1916 ATGTCAGCGTTGAACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGCACTA 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1856 CGCATGTCGCGCAAGACTGTAACCACGCGTCTGTTGACTGGCAGGTGGTGGCCAATGGTG 1915
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                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 ctcctcccgtgtgtgtgactcgcagaacgaatgtgtaggttgggctgggtgtggcttattctg 82
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TOPOLOGY: c1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                           COUNTRY:
                                                                                                                                                                                            CITY: Seattle
                                                                                                                                                                                                               STREET:
                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
   APPLICATION NUMBER: FILING DATE: 25-JUI
                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cggtggtggatgttatcagggcagcggcgcatgaaggagtttacatagaacccgaagcca 142
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                                                                                                                                            98104-7092
                                                                                                                                                                            Washington
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                                                                                                                                                                                                               6300 Columbia Center,
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                                                                                                                                                                                                                                 SEED and BERRY LLP
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25-JUN-1997
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                                                                                                                                                                                                                                                                                                                     Katherine J.
                                                                                                                                                                                                                                                                                   GLUCURONIDE REPRESSORS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3094 - 3378: 3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA nopaline synthase gene 3379 - 5642: pUC18 derived sequence ampicillin resistance to the bacterium
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1285 - 3093: coding sequenc
3094 - 3378: 3' regulatory
                      US/08/882,704A
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Pred. No. 2;
0; Mismatches 70; Indels
                                                                                                                                                                                                                 701 Fifth Avenue
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Best Local (
                                              TELEFAX: (703) 836-202
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
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STRANDEDNESS:
                                                                                                  TELEPHONE:
                             ENGTH:
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              : 14683 base pairs nucleic acid
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Sequence 1, Application US/08819866 Patent No. 5830698 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER: 39.317
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                   APPLICATION NUMBER: US/06 FILING DATE: 14-MAR-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: REFF, Mitchell E.
PPLICANT: BARNETT, Richard Spence
PPLICANT: MCLACHLAN, Karen Retta
                                                                                                                                                                                                          MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release
TREETER: Patentin Release
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Local Similarity 50.4%;
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                                         NAME: Teskin, Robin L. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                    E: BURNS, DOA
P.O. Box 1404
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(703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME .
                                                                                                                                                                                                                                                                                                                                                                                                                                        DOANE, SWECKER & MATHIS, L.L.P.
                                                                                                                                                                                us/08/819,866
                                                                   35,030
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Pred. No. 2.4;
0; Mismatches
                                                   012712-352
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US-08-819-866-1

DNA (genomic)

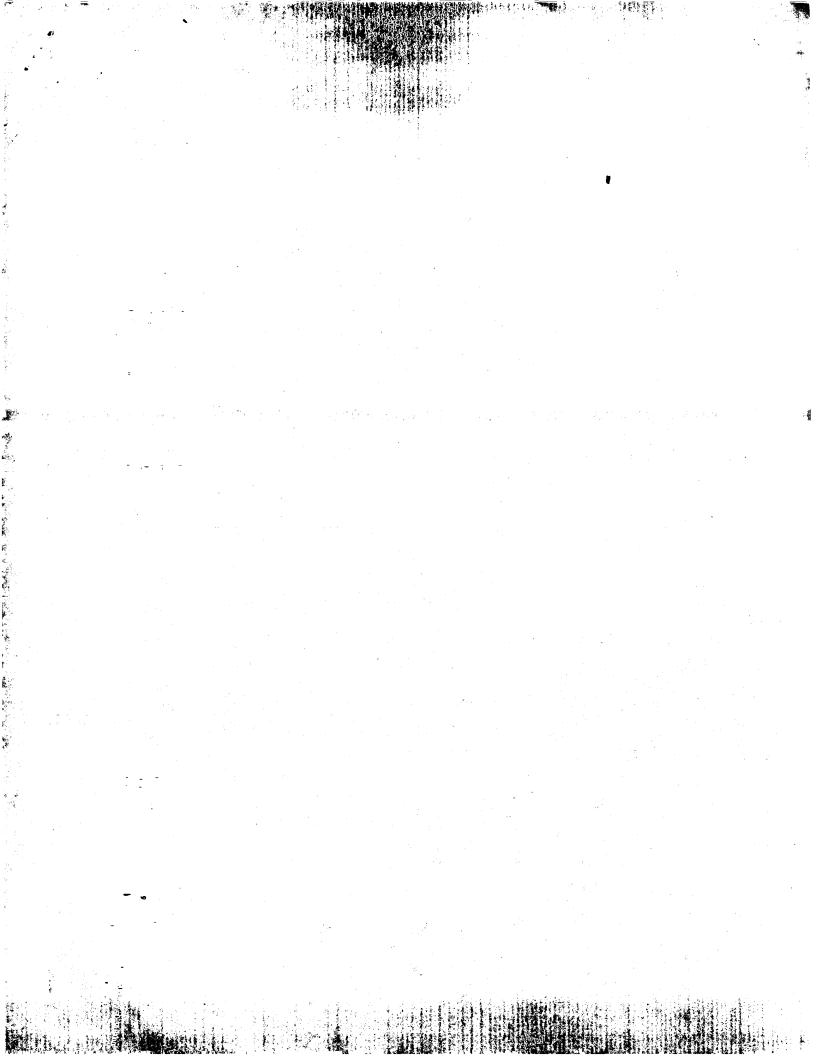
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US-09-023-715-1/c
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               Query Match

Best Local Similarity

Matches 71; Conserv
                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                        NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE_DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.4%;
Matches 71; Conservative
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentingRelease #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/819,866
FILING DATE: 14-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7509 ATGTCAGCGTTGAACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGCACTA 7450
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                                                                                                                                         STRANDEDNESS:
TOPOLOGY: 111
                                                                                                                                                                      LENGTH: 14683 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Alexandria
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22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: BURNS, DOANE, SWECKER & MATHIS, L.L.P. P.O. Box 1404
               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCIACHIAN, Richard Spence
MCIACHIAN, Karen Retta
VENTION: RETHOD FOR INTEGRATING GENES AT
VENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
VENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
                                                                                                                                           linear
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                                                                                                                 DNA (genomic)
                                                                                                                                                         single
                            8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/09/023,715
             0;
     Score 29; DB 4; Length 14683;
Pred. No. 3.4;
0; Mismatches 70; Indels
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Pred. No. 3.4;
0; Mismatches
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Search completed: June 23, 2000, 09:51:55 Job time: 6701 sec



GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Title: US-09-214-478-4

Sequence: 1 MVLPALIPAPPVCDSQNECVG......SIWHE

Searched: BLOSUM62
Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

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IGG-Fc binding pro-
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                                                                                       Streptococcus pneu
BtI109P insecticid
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WO9088
ID WO AC WO
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DE HC
KW Ce
KW CP
FPN 115
PF 113

W09088 standard; Protein; 394
W09088;
03-JUL-1997 (first entry)

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Homo sapiens. EP-748868-A2.

18-DEC-1996. 13-JUN-1996; 109447. 15-JUN-1995; JP-188472. (RIKA) INST PHYSICAL & CHEM RES.

经额

Human ceramide glucosyltransferase.
Ceramide glucosyltransferase; GlcT-1; glycosphingolipid biosynthesis; glycosylation; glycosphingoceramide; glucosyleramide; human.

P 64	Ag Ad	Z M O	00 00 00 00	8 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	PROBRE	R D R R R R R R R R R R R R R R R R R R	RESUL P8067	
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80 ARTWFC	23 GVAYSA : 291 GVFEAI	Matc Local	pathogenesis. See also P821 Sequence 52	Identifying pathogenic gene Claim 1; Page 12; 19pp; Eng The ntrA gene product is a processes of nitrate assimi C4-dicarboxylate transport, DCtD resp. It can also be	29-MAY-1987; US-05; (GEHO-) Gen Hospita Ronson C. Ausubel I WPI; 88-339561/48. N-PSDB; N81266. Cloned rhizobium mo	74 st 74; 74; Gene gene ; sig tion; tion; obium 92984 92984	. 1	56.55
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ARTWFCFRKYDYVRRSIWHDTTINTISVVSAHSVQ 	GVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREWIYYNYYTERSKRRDRRRRSVCH	Score 68; Pred. No. 20; Mismat		s. lish. transcrip lation, s lation, s working used to d	A ge	tein; 523 AA. entry) transcriptional aci ; C4-dicarboxylate		W35562 W09819 W74802 W35565 W43394 W44302 R44929 R54921 R54921 R54921 R54921 R54921 R54921
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Best Local Similarity
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08-SEP-1998; U18638.
22-SEP-1997; US-059725.
08-SEP-1997; US-059180.
(UYPR-) UNIV PRINCETON.
Cong J, Schenk T, Zhu H;
WPI; 99-243729/20.
                                   New isolated human genes
Claim 5; Page 174-176; 184pp; English.
This sequence is encoded by a human gene of the invention, repressed in the presence of tem infection, designated HCMV-repressible genes (crg o crgs). The invention also relates to genes that are induced to express b both HCMV and interferon (IFN), designated HCMV-inducible genes (cig or cigs). The products can be used to obtain agents which can be used for anti-viral therapy, particularly anti-HCMV therapy. They can also be used for the development of drugs that would allow for higher dosage IFN treatments without the concomitant toxicity normally associated with administering high levels of IFN. The products can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a novel ceramide glucosyltransferase (GlCT-1), which has catalytic activity for glucose transfer from UDP-glucose to ceramide. Ceramide glucosyltransferase catalyses the first glycosylation step of glycosylingoceramide to produce glucosylceramide, a precursor to more than 300 glycosphingolipid biotechnology areas as laboratory agents, and also as preparatory gagents, for the manufacture of pharmacological active substances. It is expected to have use in therapeutic and preventive treatment of diseases based on reduced expression of ceramide
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human HCMV repressible gene protein, SEQ ID NO 35.

HCMV repressible gene; crg; human; human cytomegalovirus; interferon; HCMV therapy; detection; diagnosis;
                                                                                                                                                                                                                                                     N-PSDB; X33956.
                                                                                                                                                                                                                                                                                                                                                                                                                              drug screening.
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WPI; 97-036152/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05381 standard; Protein; 394 AA.
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                                 for
                              detection, diagnosis and drug screening
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                                        IgG-Fc binding protein.
Fragment 13; pNV11-ST; IgG-Fc binding human; colonic epithelium; monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                     DNA derived from colonic epithelium encoding IgG-Fc binding protein used in the mapping and analysis of IgG-Fc binding protein mRNA Claim 1; Page 71-84; 132p; Japanese.

This sequence is encoded by fragment 13 which is a NotI/KpnI fragment from pNVII-5T. This sequence represents a portion of the IgG-Fc binding protein of human colonic epithelium. This sequence was used in the isolation of the full length sequence given in W14749. mRNA isolated from human colonic epithelial tissue was used to prepare a cDNA library. This was screened using monoclonal antibodies K9 and K17 which bind to the large and small components of the binding protein. Pactive clones, see also TG3077-81, were used to derive probes for screpning a second DNA library from human colonic epithelial tissue.
                                                                                                        W14749 standard; Protein; W14749;
              Homo sapiens.
WO9527057-A1.
                                                                                                                                                                                                      1604
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                                                                         13-MAY-1997 (first entry) igG-Fc binding protein.
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N-PSDB; T63073.
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13-MAY-1997
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30-MAR-1995;
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03-APR-1995;
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WO9527057-A1.
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JP-222547.
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27.7%;
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7; Mismatches 26;
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                                          protein; immunoglobulin;
antibody; K9; probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding
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PT New modified butyrophilin - not cross-reactive with myelin proligo-dendrocyte glycoprotein useful in dairy products, vaccines, products assays for susceptibility to multiple sclerosis

PS Disclosure; Page 46-47; 53pp; English.

CC. This polypeptide comprises the rat myelin oligodendrocyte production (MGG). The invention relates to butyrophilin (BTN, CC. See W97812-16), a major component of the milk fat globule membrane component of BTN has a high degree of identity with the Igv component of the immunoglobulin (Ig) superfamily. The intermediate membrane component of BTN has a high degree of identity with the Igv component of antibodies which cross-react with endogenous MGG, and component of antibodies which cross-react with endogenous MGG, and component of antibodies which cross-react with endogenous MGG, and component to MGG, e.g. by removing or modifying the IgI domain of a component of the endogenous BTN (nham) in a diary product, or by producing a numanised chimeric BTN. The invention includes genetic manipulation cof the endogenous BTN gene of an animal such that the human IgI component of the endogenous BTN gene of an animal such that the human patient from the component of the subman patient from the component of the component of the component of the milk. Methods are component of the component of the subman patient from the component of the subman patient from the component of the component of the subman patient from the component of the component
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W97817
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA derived from colonic epithellum encoding IgG-Fc binding protein used in the mapping and analysis of IgG-Fc binding protein mRNA Claim 3; Page 86-113; 132p; Japanese.

This sequence represents the IgG-Fc binding protein of human colonic epithelium. This sequence was isolated using the sequence given in w14748. mRNA isolated from human colonic epithelial tissue was used to prepare a cDNA library. This was screened using monoclonal antibodies K9 and K17 which bind to the large and small components of the binding protein. Active clones, see also T63077-81, were used to derive probes for screening a second DNA library from human colonic epithelial tissue. Sequence 5405 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-APR-1995; J00638.
01-APR-1994; JF-129487.
24-AUG-1994; JF-222547.
30-MAR-1995; JF-109927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat myelin oligodendrocyte glycoprotein.
Myelin oligodendrocyte glycoprotein; MOG; rat; butyrophilin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linington C, Mather IH; WPI; 99-142845/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple sclerosis; diagnosis; vaccine;
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(UXMA-) UNIV MARYLAND E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALSAPPQC -- QDGCAEGCQCDSGFLYNGQACVPIQQCGCYHNGVYYEPEQTVLID---
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Pred. No. 4e+02;
7; M1smatches
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in its milk. Methods are to MS in a human patient from patient at risk of developing
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Best Local Similarity
Matches 15; Conserv
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27-FEB-1998; 008258.
10-JUL-1997; DE-029490.
28-FEB-1997; DE-008134.
(EVOT-) EVOTEC BIOSYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a pathogenic autoimmune resp
possible, by screening the p
gene with domains which are
Hydra head activator binding protein - useful in screening assay for agonists or antagonists. Claim 3; Page 6-11; 21pp; German.
This sequence represents a head activator binding protein isolated from Chlorchydra viridissima by chromatographic methods. The protein is used in a screening assay for agonists or antagonists comprising determining the binding properties of candidate substances with the protein. The assay can be used to screen for substances useful for treating neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydra head activator binding protein. Head activator binding protein; hydra; scantagonist; treatment; neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W76041 standard; Protein; 1661 W76041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domains (claimed).
Sequence 150 AA;
                                                                                                                                Hampe W, Schaller C;
WPI; 98-468562/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
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                                                                                                                                                                                                                                          Domain
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/note= "As given
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1003. .1041
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ng protein; hydra; screening assay; agonist;
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                                                                                                                                                          GMBH
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; Pred. No. 5.8;
5; Mismatches
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Query Match
Best Local Similarity
Matches 21; Conserv

Conservative

9.9%;

Score 61.5; DB 1; Pred. No. 1.2e+02; 4; Mismatches 25;

Length 1661;

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17;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maize dwarf mosaic virus polyprotein MDMV-B; viral resistance; disease res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W10344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPYCDSQNECVGWL----GVAYSAVVDVIRAAAHEGYYIEPEARGRLDALR-----E
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843
                                                 /note-
1362
                                                                         /note-
1346
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852
                                                                                                                        /note= "unidentified 847
                                                                                                                                                                         /note= "unidentified 834
                                                                                                                                                                                                 /note- "unidentified 829
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                          /note- "unidentified 2077
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/note= "portion of the helper component-P2
proteinase"
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'note= "conserved motif characteristic
                                                                                                                                                                                                                                                                                    'label- Coat_protein
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note= "claimed polypeptide (Claim 20)"
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ote= "claimed polypeptide (Claim 20)"
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              "unidentified
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Best Local
               N-PSDB (23349.

N-PSDB (23349.

N-PSDB) (23349.

Synthetic specific binding agent and reshaped human antibody specific for human polymorphic epithelial mucin for treatment and in-wivo diagnosis of pen-producing cancers

Claim 11; Fig 12; 62pp; English.

The reshaped antibody sequence was deduced from the sequence of a reshaped human variable heavy chain gene which had a human class I framework but contained mouse CDRs. To reshape a human heavy chain framework but contained mouse CDRs. To reshape a human heavy chain
                                                                                                                                                                    W09204380-A.
19-MAR-1992.
05-SEP-1991; G01511.
07-SEP-1990; GB-019553.
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20-JUN-1996;
30-JUN-1995;
                                                                                                                                 Verhoeyen M;
WPI; 92-114305/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2313
                                                                                                                                                                                                                                                                                  protein
           form gene HuVHlconHMFG1.
                                                                                                                                                            (UNIL ) UNILEVER PLC
                                                                                                                                                                                                                                               region
                                                                                                                                                                                                                                                                                                                                                                                                        R22421 standard; Protein; R22421;
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Dietz JM, Law MD;
                                                                                                                                                                                                                                                                                                                      region
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produce a plasmid
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       one contg. a murine CDR, were assembled to
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transformation of E.

22222

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29-JUL-1992 (first entry)
Antibody produced from HuVHlconHMFG1
Anti-HMFG specificity: commlement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to a truncated protein (pref. smaller than 200 amino acids), no translation of mRNA occurs or the transcribed mRNA lacks the translation initiation codon or includes a premature stop codon. Expression of the chimaeric gene inhibits infection of plants (p: sorghum, sugarcane, esp. maize) by MDMV. The transgenic plants display an inheritable resistance trait.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral protein
Claim 20; Page 31-44; 64pp; English.
The sequence of the polyprotein encoded by the polycistronic mRNA
(T47073) of maize dwarf mosaic virus strain B (MDMV-B) is given in
W10344. New chimaeric genes comprise a monocotyledonous plant
promoter linked to a modified nucleic acid sequence derived from
the MDMV-B genome. The modification is such that mRNA is translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wPI; 97-108965/10.
N-PSDB; T47073.
Chimaeric gene for imparting
sequence modified to express
                                                                                                                                                                                                                                                                               human milk fat globule; polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 RAAAHEGVYIEPEARGRLDALREWIYYNYYTERSKRRDRRRRSVCHA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGIKYEGIYIPKLEKERIVAILEW-----DRSNLPEHRLEAICAA 2352
                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                             complementarity determining re
; polymorphic epithelial mucin;
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                                                                                                                                                                                                                                                                                                                                                                                                            118
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                                                                            mouse heavy chain'
                                                                                                                                                      mouse heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 61.5; DB 1;
Pred. No. 2.3e+02;
9; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          viral resistance non-translatable
mouse heavy chain'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2763;
                                                                                                                                                                                                                                                                               region;
in; PEM.
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R54758 10
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Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The antibodies produced are essentially human so are unlikely to cause adverse reactions. The reshaped molecule can be used to treat PEM-producing cancers (e.g. of the breast, ovary, uterus or lung) and in in-vigo diagnosis.

See also R22419-22.

Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Enumanised HMFG1 heavy chain variable region.
Esingle chain Fv fragment; ScFv; Gene Therapy; Monoclonal Antibody;
Human Milk Fat Globule antigen; HMFG1.
                                                                                                                                                                                                                      /label- humanised misc_difference 67. .68 /label- humanised
                                                                                                                                                                                                                                                                                                                                                                    misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                   misc_difference
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97
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                                              /label=
118
                                                                                                                         /label- humanised
87
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                 1. .118
/label-
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  /note=
1. .30
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23.2%; Pred. No.
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          humanised HI
"heavy chain
                                      humanised by replacing Ala with Ser
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                    HMFG1
          #FG1 monoclonal antibody
variable region"
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                                                        Pro with
                                                                            Ser with Ala
                                                                                               Ser with Thr
                                                                                                                  Thr with Arg
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CCC PFI DIA PF
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Best Local Similarity
Matches 23; Conserv
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04-NOV-1993;
04-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMCR ) IMPERIAL CANCER R
Epenetos AA, Spooner RA;
WPI; 94-167477/20.
N-PSDB; Q64819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09410323-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virus with modified binding moiety specific for the target cells
- used to deliver genes for gene therapy and cancer treatment
Example 4; Page 74; 110pp; English.
Example 4; Page 74; 110pp; English.
R54758 showes an humanised HMFGI heavy chain variable region. The
mouse HMFGI is changed at specific residues within the framework region.
It is used to generate an SCFV with the humanised HMFGI light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region
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                                                                                                                                                                                                                                                                                                                                                               Human secreted protein encoded by 5' EST SEQ ID NO: 142.
Human, secreted protein; EST; expressed sequence tag; djagnosis;
forensic; gene therapy; chromosome mapping; signal peptide;
upstream regulatory sequence; cytokine activity; cell proliferation;
differentiation; haematopoiesis regulation; tissue growth regulation;
reproductive hormone regulation; chemokactic; chemokinetic; haemostat:
thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy.
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The invention is concerned with the fusion fibre such that the fusion sequence can be
N-PS(DB; X51928.)
N-PS(DB; X51928.)
New isolated brain-derived nucleic acids - used to develop per which may have cytokine, immune, regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity (Claim 34; Page 522-523; 577pp; English.
X51787 to X52019 represent 5' expressed sequence tags (ESTs)
                                                                                                                                                   (GEST ) GENSET.

Duclert A, Dumas Milne Edwards
WPI; 99-153782/13.
                                                                                                                                                                                                                                 31-JUL-1998; IB1236
01-AUG-1997; US-905:
                                                                                                                                                                                                                                                                                                            Homo sapiens.
WO9906552-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y13128 standard; Protein; 133
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GB-023084.
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                                                                                                                                                                                                                                    US-905223.
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31. .35
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108. .118
/label= FR 4
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  sequence tags (ESTs) for human
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                                                                                   Query Match
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Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC secreted proteins, and encode the proteins given in x12987 to x13219, CC respectively. The proteins given represent the signal peptide and an CC N-terminal fragment of a secreted protein. The nucleic acid sequences CC can be used for producing secreted human gene products. They can also CC be used to develop products for diagnosis and therapy. The proteins CC obtained may have cytokine activity, cell proliferation/differentiation CC activity, hemmatopoiesis regulating activity, tissue growth regulating CC chemokinetic activity haemostatic and thrombolytic activity, receptor/CC ligand activity, anti-inflammatory activity, tumour inhibition activity cor other activities. The products can be used in forensic, gene therapy CC and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or Sequence 133 AA;
                                                                                                                                                                                                                                                                                         11 MAR-1998:
26-AUG-1997; 306501.
13-DEC-1996; US-032875.
06-SEP-1996; US-025436.
06-SCT-1996; US-027873.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Browne MJ, Clinkenbeard HE, Creasy CL, Ka
Livi GP, Southan CD;
WDI; 98-161101/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; V29522.

Nucleic acids encoding human serum protease protein(s) - used diagnosing pre-disposition to Alzheimer's disease, etc. Example 2; Page 18-19; 65pp; English.

The sequence is that of at least a fragment of the serine protease PSP1. This can be used to identify modulators of serine protease activity and also to diagnose a condition associated with lack of one of the serine proteases or a genetic predisposition to neurodegeneration in a patient, preferably predisposition to Alzheimer's disease.

Sequence 323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      *Homo sapiens PSP1 partial sequence.
PS-1; presentlin; presentlin-1; PSP-1; Alzheimer's disease; serine protease; neurodegeneration; predisposition; diagnos
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
EP-828003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-1998
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                                                                                   Local Similarity 32.0 Local Similarity 32.0 Local Similarity
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                                                      2 VLPALPAPPVCDSQNECVGWLGVAYSAVVDVIRAAAHEGVYIE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 YAYHVEREKERDPEHRALCDLGPW 55
                          YNYYTERSKRRDRRRRSVCHARTW 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                              9.78;
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41.78;
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                                                                                                Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 60; DB Pred. No. 8.6;
                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         predisposition; diagnosis
                                                                                                                                                                                                                                                                                                                         Karran
                                                                                                           DB 1;
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                                                                                  13; Indels
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                                                                                                           Length 323;
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Query Match 9...
Best Local Similarity 32.6
Matches 14; Conservative
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26-AUG-1997; 305501.
13-DEC-1996; US-032875.
06-SEP-1996; US-02436.
25-OCT-1996; US-027873.
25-OCT-1996; US-027873.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Browne MJ, Clinkenbeard HE, Creasy
Livi GP, Southan CD;
WPI; 98-161101/15.
                                 New polypeptide(s) involved in cobalamin and cobamide biosynthesis - and DNA encoding them, for amplification of cobalamin, esp. coenzyme B12 prodn, Claim 17; Fig 16; 299pp; French.

This sequence corresponds to one of 24 polypeptides obtained from p. dentrificans and implicated in the biosynthesis of cobalamines and/or cobamides, specifically in catalysing the transfer of a methyl group to positions C1, C5, C11, C15 or C17 in the conversion of precorrin-3 to cobyrinic acid a, c-diamide. It is encoded by part is the 8.7kb EcoRI-EcoRI fragment of plasmid pXL367. The plasmid was insolated from a P.denitrificans genomic DNA bank constructed in
                                                                                                                                                                                                                                                                                                                                                                                                                      Blanché F, Meron B, Crouzet J, Debussche L, Levy-Schil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P.denitrificans COB L. cob gene; corrinoid; descobaltocorrinoid; cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R13506 standard; Protein; 413
R13506;
25-OCT-1991 (first entry)
vector pXL59.
See Q13284-Q13288.
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31-JAN-1990; FR-001137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas denitrificans.
WO9111518-A.
08-AUG-1991.
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Nucleic acids enoding human serum protease protein(s) - us diagnosing pre-disposition to Alzheimer's disease, etc. Claim 7; Page 41-42; 65pp; English.

The sequence is that of the consensus sequence of PSP1-3 serine protease which can be used to identify modulators of serine protease activity and also to diagnose a condition associated with lack of one of the serine proteases or a genetic predisposition to neurodegeneration in a patient, preferably predisposition to Alzheimer's disease.

Sequence 377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RHON ) RHONE-POULENC BIOCH.
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Homo sapiens PSP1-3 consensus sequence.
PS-1; presenilin; presenilin-1; PSP1-3; Alzheimer's disease; serine protease; neurodegeneration; predisposition; diagnosis.
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13-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VLPALPAPPVCDSQNECVGWLGVAYSAVVDVIRAAAHEGVYIE
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RESULT W56774 ID W56

13

W56774 standard; Protein; 377 AA.

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Search completed: June 23, 2000, 10:03:38 Job time: 3366 sec
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PA 13-DEC-1996; US-032875.

PR 13-DEC-1996; US-023436.

PR 06-SEP-1996; US-025436.

PR 06-SEP-1996; US-025436.

PR 06-SEP-1996; US-025436.

PR (SMIK ) SMITHKLINE BEECHAM PLC.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

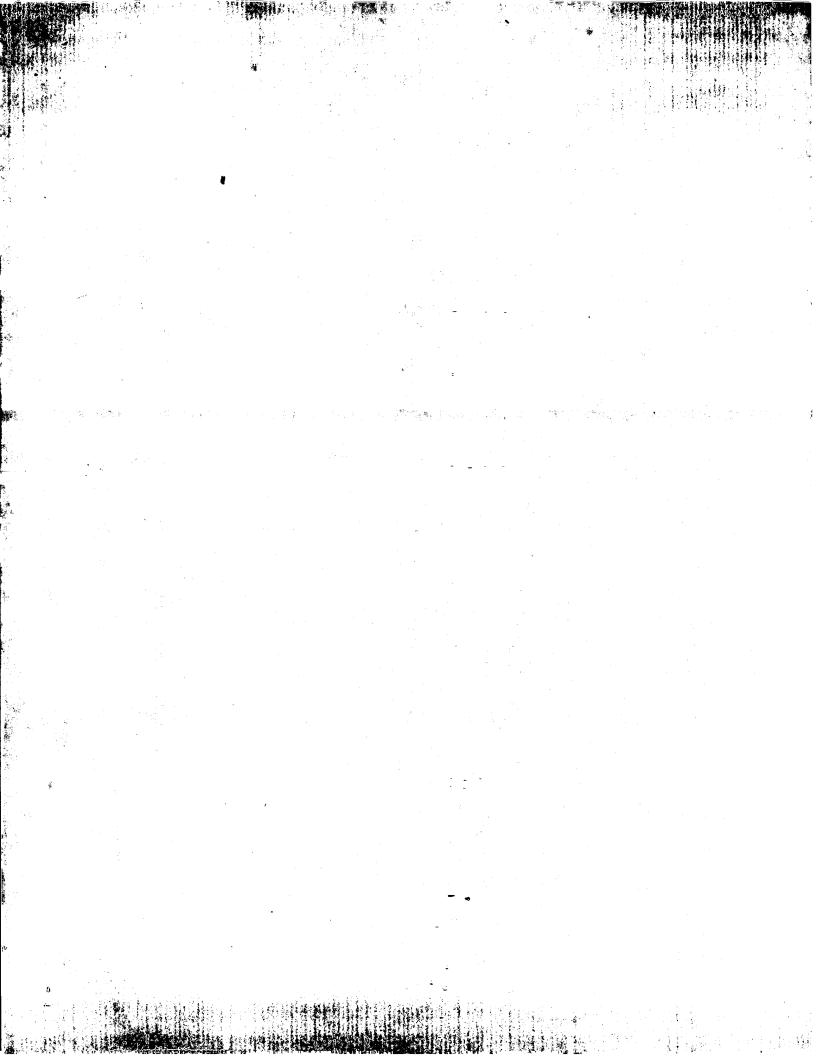
PI Browne MJ, Clinkenbeard HE, Creasy CL, Karran EH,

PI Livi GP, Southan CD;

PR WPI; 98-161101/15.

PR NPSDB; V29538.

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Matches 17; Conservative
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Homo sapiens PSP1-4 consensus sequence.
PS-1; presenilin; presenilin-1; PSP1-4; Alzheimer's disease; serine protease; neurodegeneration; predisposition; diagnosis.
Homo sapiens.
EP-828003-A2.
                                                                                                                                                  Pred. No. 34;
2; Mismatches
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Perfect score: Sequence:

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Sequence

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Minimum DB seq length: 0
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score greater than or equal to the score of the result being pr
and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0
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621
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/5COMB.pep:*
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US-08-860-1174A-12

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US-08-471-113A-2

US-08-471-113A-2

US-08-471-1155-42

US-08-18-914-4

PCT-US93-1055-42

US-08-918-914-6

US-08-18-914-6

US-08-18-137-210A-1

US-08-18-432-16

US-08-331-398A-19

US-08-331-398A-19

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PCT-US96-10521-9

PCT-US96-10521-9

PCT-US96-10521-9
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US-08-483-101-14
US-08-860-174A-4
US-08-659-251-8
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US-08-496-944-2
US-08-428-257A-78
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Sequence 4, Appli
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US-08-663-713A-2
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                                                                                          Matches
                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WOTGPEFCT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/6
FILING DATE: June 14, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            ATTORNEY_AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Wenuer STREET: 805 Fiftee CITY: Washington STATE: D.C.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
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ADDRESSEE: Wenderoth,
STREET: 805 Fifteenth
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                    284 LPATIICEPISECFVASLIIGW--
                                                                                                                                                                                                                    LENGTH: 394 amino acids TYPE: amino acid STRANDEDNESS: single
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                                                      6 LPAPPVCDSQNEC-----VGWLGVAYSAVVDVIRAAAHEGVYIEPEARGRLDALREWIY 59
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/ENTION: CERAMIDE GLUCOSYLTRANSFERASE
                                                                                            Conservative
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US-08-249-112-4
PCT-US95-06556-4
US-08-386-727-4
US-08-386-727-4
US-08-39-057-14
US-08-438-562-36
US-08-438-562-36
US-08-438-5288-100
US-08-489-733-6
US-08-489-733-6
US-08-489-733-5
US-08-380-491A-2
                                                                                            10;
                                                                                        Score 63; DB 1
Pred. No. 6.8;
10; Mismatches
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76;

Gaps

VFRWDI 315

Result

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US-08-428-257A-78
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Best Local Similarity 29.0
                                                                                                                                                                                 Sequence 78, Application US/08428257A Patent No. 5885808
                                                                                                                                                                   GENERAL . INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Law, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: (
NFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTECS:
LENGTH: 2763 amino acids
TYPE: amino acid
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                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                    2313 RGIKYEGIYIPKLEKERIVAILEW-----DRSNLPEHRLEAICAA 2352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 MVFF---
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                                                                                                                                                                                                                                                                                                                    34 RAAAHEGVYIEPEARGRLDALREWIYYNYYTERSKRRDRRRRSVCHA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
COUNTRY:
                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: CIBA-Geigy Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 YNYYTERSKRRDRRRRSVCHARTWF-
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              New York
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                                                                                                                                             Spooner, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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                                                                                                                                                                                                                                                                                                                                                                      9.9%;
                                                                                                               Compounds to
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                                                                                                                                 A.A.
                                                              Goldberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/496,944
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                                                                                                                                                                                                                                                                                                                                                      Score 61.5; DB 3;
Pred. No. 1.3e+02;
9; Mismatches 17
                                                                                                              target cells
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                                                                                                                 COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,441B
FILING DATE: 18-DEC-1997
CLASSIFICATION: 800
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 23; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
                                                     NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MEC
TELECOMMUNICATION INFORMATION:
                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Kitchell, Barbara
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Arnold, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: Romano, Charles ITLE OF INVENTION: INSECT
                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 77210
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                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 GVAYSAV-VDVIRAAAHEGV---
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FILING DATE: 07/05/95
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0. 602303
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                                                                                                                                                                                                                                                                                                                                                                      P.O. Box 4433
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                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kulesza, Caroline A. Walters, Frederick S. Slatin, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brussock, Susan M
Malvar, Thomas M.
Bryson, James W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Von Tersch,
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                                          512/418-3000
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                                                                            MECO: 151
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Pred. No.
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                                                                                                                                                                                                               Version #1.30
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                                                                           Query Match
Best Local Similarity
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       TELEPHONE: (303) 499-8080
                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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488 MGWSGCYESYSASLSIPVKGWNSTLAYSNTY--STSVYRYDAVSEYVPYYYYKGRTKR 543
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                          19 VGWLGV--AYSAVVDV-----IRAAAHEGVYIEPEARGRLDALREWIYYNYYTERSKR 69
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/483,101 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                       NAME: Ferber, Donna M.
REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                       890 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caron, Judy
                                                                                                                                                                                          unknown
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                                                                           9.48;
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                                                                           Score 58.5;
Pred. No. 71;
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Pred. No. 41;
                                                            Mismatches
                                                                                          DB 2;
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                                                                                        Length 890;
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                                                                                                                                                                             SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: MS WORD, WINDOWS 95, V.
CURRENT APPLICATION DATA:
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LENGTH: 135 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/
FILING DATE: June 16, 1997
PRIOR APPLICATION DATA:
       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                     UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                         125 -- WGQGTTVTVS 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                           95 SIWHDTTTNTIS 106
                                                                                                                                                                                                                                                                                                                                                                               68 EWIGYIYPYNDGTKYNEKFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCSRRFDY--- 125
                                                                                                                                                                                                                                                                                                                                                                                                                   56 EWIYYNY-----YTERSKRR----DRRRRSVCH-----ARTWFCFRKYDYVRR 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: October
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San Francisco
                                                                                          INVENTION:
                                                                                                                                                                                                               pplication US/08659251
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                                                                   Poeschla, Eric
VENTION: Isolation of No.
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                                                                                                                      Wong-Staal, Flossie
Talbott, Randy
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VAN DER LOGT, Corr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERHOEIJEN, Martine Elisa
                                                                                                                                                            Kraus, Guenter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           October
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.2%;
25.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 57; DB Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                      5883081el HIV-2 Proviruses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 135;
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Sequence 8, Application PC/TUS9611445 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches .. 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  -US96-11445-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60,
FILING DATE: 26-UU-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   st Local Similarity
                                                                                                                                                                                                                                                   STREET: 201 ...
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 VCDSQNECVGWLGVAYSAVVDVIRAAAHEGYYIEPEARGRLDALREW-----IYYNYYTE 65
                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                             ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION
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TELECOMMUNICATION INFORMATION:
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                                                  ATTORNEY/AGENT INFORMATION:
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                                                                      APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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REFERENCE/DOCKET NUMBER:
              NAME: Berliner, Robert REGISTRATION NUMBER: 20,121
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                                                                                                                                                                                                                                                                                                       201 N. Figueroa Street,
                                                                                                                                                                                                                                                                                                                                                                          The Regents of the University of California VENTION: Isolation of Novel HIV-2 Proviruses
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                                                                                                                                                                                                                                                                                                                        Robbins, Berliner & Carson
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; MOLECULE TYPE: US-08-860-174A-12
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INFORMATION FOR SEQ ID NO:
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                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              APPLICATION NUMBER: US/08/860,174A
FILING DATE: June 16, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95307332.7
                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD, WINDOWS 95, V
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                              FILING DATE:
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                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UNITED STATES
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                                                                     274 amino acids
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VAN DER LOGT, Cor
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                                                                                                                                                               October
                                                                                                                        October 16, 1995
MBER: PCT/EP/96/03605
August 14, 1996
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/er. 4.0
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Best Local Similarity 25.0
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TRESULT 11
US-08-596-405-4
; Sequence 4, Application US/08596405
; Patent No. 5858706
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Best Local Similarity
Matches 23; Conserv
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TELECOMMUNICATION INFORMATION: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/296,014A
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LENGTH: 1019 amino aci
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MEDIUM TYPE: Floppy disk
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                                                                                                     418
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TLE OF INVENTION:
TLE OF INVENTION:
TLE OF INVENTION:
                                                                                                                                      80 ARTWECERKYDYVRRSI------WHDTTTNTISVVS 109
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                                                                                                                                                                                                      21 WIGVAYSAVVDVIRAAAHEGVYIEPEARGRIDALREWIYYNYY-TERSKRRDRRRRSVCH 79
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                                                                                                    ARSF----REDYVRSSTAGKSGCPDGWFEVDENCVYVTS 452
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8110 Gatehouse Road, Suite 500 East
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0; Mismatches
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Pred. No. 1.3e+02;
Pred. No. 1.3e+02;
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Best Local Similarity
Matches 23; Conserv
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APPLICANT: Ding, Je
APPLICANT: Ho, Bow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                               418 ARSF----RFDYVRSSTAGKSGCPDGWFEVDENCVYVTS 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 WGTAIYHELSSYCRAAIHAGKL--PNSGGAVHVVNNGPYSDFLGSDLNGIKSEELKSL-- 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Murphy, Jr., Gerald M REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                80 ARTWFCFRKYDYVRRSI-----WHDTTTNTISVVS 109
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                                     COUNTRY: U
ZIP: 22042
                                                                                   STREET: 8110 Garen
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                                                                      Virginia
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8110 Gatehouse Road, Suite 500 East
                                                                                                        E: Birch, Stewart, Kolasch & Birch
8110 Gatehouse Road, Suite 500 East
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                                                       USA
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Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.2%; Score 57; 1
23.2%; Pred. No. 1
                                                                                                                                                                           The Cloned Factor C cDNA of the Singapore Horseshoe Crab, Carcinoscorpius rotundicauda and Purification of Factor C
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US-08-471-119A-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amin
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Best Local Similarity
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tent No. 5827706
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC COMPATIBLE
COMPUTER: PATENT PC-POS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,119A
FILING DATE: 06-UN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
NAME: Kassenoff Melvyn
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8474
                                                                                                                                                                                                                                                                                                               STREET: 57 ACCOUNTS OF THE STATE: New Jersey
                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
TYPE: amino acids
TYPOLOGY: 11000
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REFERENCE/DOCKET NUMBER: 177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                              COUNTRY: UZIP: 07936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 ARTWFCFRKYDYVRRSI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 WLGVAYSAYVDVIRAAAHEGVYIEPEARGRLDALREWIYYNYY-TERSKRRDRRRRSVCH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICATION NUMBER: US/08/877,620
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59 Route 10
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Weber, Gerhard
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UMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                        5827706artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.2%; Score 57; DB 2; 23.2%; Pred. No. 1.3e+02;
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                                        100-8029/CONT/CONT
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; ORGANISM: Tolypocladium niveum
; STRAIN: ATCC 34921
US-08-471-119A-2
MOLECULE TYPE:
FRAGMENT TYPE:
IS-08-379-057-31
                                                    TELEFAX: (206) 727-3601
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                 TELEPHONE: (206) 727-3670
                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/379,057
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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LENGTH: 15281 amino ac
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                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                               ELEPHONE:
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STRANDEDNESS: sir
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                                                                                       115 amino acids
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ilarity 30.5%;
Conservative
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Bajorath, Jurgen
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Pred. No. 4.5e+03;
7; Mismatches 22;
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US-08-428-197-42
                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-428-197-42
                                                                                                                                                  Query Match 9.1%; Score 56.5; DB 2; Length 115; Best Local Similarity 21.5%; Pred. No. 8.6; Matches 20; Conservative 15; Mismatches 47; Indels 1
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10555

FILING DATE: 29-CCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Howells, Stacy L.

REFERENCE/DOCKET NUMBER: FD-2630

TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 42, Application US/08428197
Patent No. 5891438
                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 42:
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APPLICANT: SILVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                              16 NECVGWLGVAYSAVVDVIR--AAAHEGVYIEPEARGRLDALREWIYYNYYTERSKRRDRR 73
90 -----DIAVYYCGRGYSY---PVWGQGTTVTVS 114
                                    74 RRSVCHARTWFCFRKYDYVRRSIWHDTTTNTIS 106
                                                                      31 NYAMSWYRQAPGKGLEWYSGISASGDTTYYADSYRGRFAISRDNFKNTLYLQMNSLRAE- 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/428,197 FILING DATE:
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STATE: California
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Search completed: June 23, 2000, 10:04:38 Job time: 2843 sec

Run

8

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Post-processing: Minimum Match 0%
Listing first 45
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Result
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Score
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138.4
35.4
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30.8
30.8
30.6
Unpublished (1997)
On NOV 22, 1999 this sequence version replaced gi:6462296.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                          AW276836 630 bp mRNA EST 03-JAN-2000 xp66g11.x1 NCI_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745380 3' similar to SW:E413_ADE02 P03240 PROBABLE EARLY E4 13 KD PROTEIN.
                           Tumor Gene Index
                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                               Eutheria; Primates; 1 (bases 1 to 630)
                                                                  Homo sapiens
                                                                                              mRNA sequence.
AW276836
                                                           Eukaryota;
                                                                                      AW276836.1 GI:6663866
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                                                                                                                                                                             Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Primates; Catarrhini; Hominidae; Homo. "
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W41762 mc5g02.r1
AI323278 mf06dl0.y
AQ162256 mgxb0012K
AQ325183 mgxb00212K
AQ325183 mgxb0021A
AQ891726 HS.3100.B
AW107119 um19a01.y
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AQ841382 T136655b
AQ841373 T136636b
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AW006018 wz91g08.x
AW163374 au94d10.y
AQ944247 Sheared D
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AI385950 mg29b06.y
AA377776 EST90394
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AW265066 xq60g03.x
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W82078 me96g07.r1
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1140104 mg93a05.r

1290263 vc90908.r

1784945 uj22a03.x

1195511 ui50g10.y

1217816 mu98g09.r

1481623 vh24d11.x

1115246 ui43a10.y
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similar to
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REFERENCE AUTHORS

COMMENT

JOURNAL TITLE ACCESSION VERSION

SOURCE KEYWORDS

ORGANISM

RESULT AW276836

DEFINITION

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aactactacacagagcgatctaagcggcgagaccggagacgcagatctgtttgtcacgcc
                                                                                                                                                                                                                                                                                                                CGCACCTGGTTTTGCTTCAAGAAATATGACTACGTGCGGCGTTGCATTTGGCATGACACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: Andrew Berchuck M.D., John Gillespie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     priming. Non-directionally cloned into the UDG sites pAMPIO. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

134 c 173 g 168 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: ovary; Vector: pAMP10; cDNA made by oligo-dT :.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2745380"
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lab_host="DH10B"
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SW:E411_ADE02 P03241 PROBABLE EARLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Possible reversed clone: polyT n
Seq primer: -40UP from Glbco
High quality sequence stp: 425.
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Possible reverse
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                         M18889 303 bp mRNA EST 10 mc044902.rl Soares mouse p3NMF19.5 Mus musculus cDNA 1MAGE:337970 5' similar to SW:RB14_RAT P35287 RAS-RAB-14. [1] ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Primates;
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 303)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                     W18889.1 GI:1294599
                                                                                                                                                                                                             house mouse.
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WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n library type
le reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: colon; Vector: pAMP10; cDNA made by oligo-dr priming. Non-directionally cloned into the UGG sites of pAMP10. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/clone="IMAGE:2755060"
/clone_lib="NCI_CGAP_CC22"
/clone_lib="NCI_CGAP_CC22"
/tlssue_type="colonic adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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98.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 138.4; DB 79;
Pred. No. 1.7e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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JOURNAL COMMENT
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                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
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DEFINITION
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AA656067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 ttattctgcggttggatgttatcagggcagcgggggcatgaaggagtttacatagaacc 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 TCAAACTGCAGATTTGGGATACAGCAGGGCAGGAGCGGTTCAGAGCGGTTACACGGAGCT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgaagccaggggggcgcctggatgctttgagagagtggatatactacaactactacacaga 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcgatctaagcggcgagaccggagacgca 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCACTTAAGCAGCTGGTTGACAGACGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA 127
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On May 9, 1995 this sequence version replaced g1:802677.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMACE Consortium (info@image.llnl.gov) for further information.
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 345)

Allen,M., Bowles,M., Dietrich,N., Dubuque,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                              RAB-14. ;, mRNA sequence.
AA656067
AA656067.1 GI:2592221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vs49h11.rl Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149669_5' similar to SW:RB14_RAT p35287 RAS-RELATED PROTEIN
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/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)
/lab_host="Site_1"
/lab_host="DH10B (ampicillin resistant)
/lab_host="Site_1"
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/db_xref="taxon:10090"
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COMMENT
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AA562033
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VERSION
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TITLE .
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Best Local S
Matches 78
                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                 ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 ACCACTTAAGCAGCTGGTTGACAGACGCA 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcgatctaagcggcgagaccggagacgca 223
           Eukaryota; Meuner Sciurognaum, Eutheria; Rodentia; Sciurognaum, Eutheria; Rodentia; Sciurognaum, I (bases 1 to 348)

1 (bases 1 to 348)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Marra, M., Hillier, L., Lacy, M., Le, M., Martin, J., Morris, M., Geisel, S., Kucaba, T., Lacy, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                              AA562033 348 bp mRNA EST 18-AUG-1997 v125e09.rl Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:973288 5' similar to SW:RB14_RAT P35287 RAS-RELATED PROTEIN RAB-14. ; mRNA sequence.
                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
On Sep 12, 1996 this sequence version replaced Contact: Marra M.Youse EST Project
WashU-HHMI Mouse EST Project
WashLigton University School of Medicinep
                                                                                                                                                                                                                                                                                               AA562033.1 GI:2333498
                                                                                                                                                                                                                                                    house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.linl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Possible reversed clone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ible reversed clone: similarity on wrong strand primer: -28m13 rev1 ET from Amersham quality sequence stop: 279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
  lished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1149669"
/clone="IMAGE:1149669"
/clone=lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
/corx; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo df. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
3'-3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
24 a 61 c 88 g 72 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345;
                                                                                                                                                                                                  Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                               Dubuque,
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AA509726
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on sep 12, 1996 this sequence version repl
Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                        1 (bases 1 to 389)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                            AA509726 389 bp mRNA EST vg20106.rl Soares mouse NDMH Mus musculus cDN 5' similar to SW:RB14_RAT P35287 RAS-RELATED
                                                                                                    The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                         EST
                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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4444 Forest Park Parkway, Box 8501, St. La
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -28m13 rev1 ET from Amersham.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Stratagene mouse Tcell
/tissue_type="Tcell"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35.4; DB 35;
Pred. No. 0.65;
0; Mismatches 71;
                                                                             replaced
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ED PROTEIN RAB-14. ;,
                                                                                                                                                                                                                                                         Murinae;
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                                                                                                                                                                                                                                                         Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 ACCACTTAAGCAGCTGGTTGACAGACGCA 361
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; mage Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W30475 453 bp mRNA EST 11-SEP-1996 mc18a09.rl Soares mouse p3NNF19.5 Mus musculus cDNA clone IMAGE:348856 5' similar to SW:RB14_RAT P35287 RAS-RELATED PROTEIN RAB-14. [1] ;, mRNA sequence.
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Similarity 52.3%;
78; Conservative
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1 (bases 1 to 453)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Unpublished (1996)
On Nov 29, 1993 this sequence version replaced g1:430269
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W30475.1 GI:1309206
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                                                                                                                                         The WashU-HHMI Mouse EST Project
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/strain-"C57BL/6J"
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/lab_host="DH10B"
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/sex="male"
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/clone="IMAGE:861923"
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Best Local (
                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: ETPrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA041778 477 bp mRNA EST 03-SEP-1996 mJ02g10.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:474978 5' similar to SW:RB14_RAT P35287 RAS-RELATED PROTEIN RAB-14. [1]; mRNA sequence.
                                                                                                                                                    Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 477)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 10.3%;
Similarity 52.3%;
Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Jun 18, 1996 this sequence ver
                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA041778.1 GI:1520067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="PH10B (ampicillin resistant)"
/lab_hos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ထ
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a 89 c 100 g 109 t
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/clone 14b="7-
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Mammalia;
Sciurognathi; Muridae; Murinae; Mus.
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        sequence version replaced g1:1366624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35.4; DB Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71;
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FEATURES

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.Best_Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 TCAAACTGCAGATTTGGGATACAGCAGGGCAGGAGCGGTTCAGAGCGGTTACACGGAGCT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 ttättotgoggtggtggatgttatcagggcagoggcgtgaaggaggtttacatagaacc 134
                                                                                                                                                                                                                                                                                                                                                                                       195 gcgatctaagcggcgagaccggagacgca 223
                                                                                                                                                                                                                                                                                                                                                                                                                         371 ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 cgaagccagggggcgcctggatgctttgagagagtggatatactacaactactacacaga 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                        431 ACCACTTAAGCAGCTGGTTGACAGACGCA 459
         Marra, M., Hillier, L., Geisel, S., Kucaba, T.,
                                                                                                                                                                                                            W82078 479 bp mRNA EST 12-SEP-1996 me96907.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:403452 5' similar to SW:RB14_RAT P35287 RAS-RELATED
                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 479)
                                                                                                         Mus musculus
                                                                                                                                                                                    PROTEIN RAB-14. [1] ;, mRNA sequence W82078
                                                                                                                                                                 W82078.1 GI:1539549
                                                                                                                           wouse mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
WashG-HHMI Mouse EST Project
WashIngton University School of Medicinep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: similarity on wrong strand Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l: mouseest@watson.wustl.edu clone is available royalty-free through LLNL; contact the Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 286 1800
314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ. from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:474978"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="Soares mouse embryo NbME13.5 14.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35.4; DB Pred. No. 0.74; 0; Mismatches
   Alien, M., Bowles, M., Dietrich, N., Dubuque, T., Lacy, M., Le, M., Martin, J., Morris, M.,
                         Allen, M.,
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                       Bowles, M.,
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                                                               Mus
                                                                               Mammalia;
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VERSION
KEYWORDS
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COMMENT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                       10
                                 AA874208
AA874208.1
house mouse
                                                                           RAB-14.
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ORIGIN

BASE COUNT

REFERENCE

KEYWORDS VERSION

ORGANISM

ACCESSION

AUTHORS

RESULT W82078

DEFINITION

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208 ACCACTTAAGCAGCTGGTTGACAGACGCA
                                                                                                                                                                                       195 gcgatctaagcggcgagaccggagacgca 223
                                                                                                                                                                                                                                                                                                                                       75 ttattctgcggtggtggatgttatcagggcagcggcgcatgaaggagtttacatagaacc 134
                                                                                                                                                                                                                            ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA
                                                                                                                                                                                                                                                      ogaagocaggggggcgcctggatgctttgagagagtggatatactacaactactacacaga 194
                                                                                                                                                                                                                                                                                                       TCAAACTGCAGATTTGGGATACAGCAGGGCAGGAGCGGTTCAGAGCGGGTTACACGGAGCT 147
          vx03g04.rl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1263414 5' similar to SW:RB14_RAT p35287 RAS-RELATED PROTEIN
                                                            AA874208
                                                                                                                                                                                                                                                                                                                                                                                            78; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1393029.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Possible reversed clone: similarity on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer: -28M13 rev2 from Amersham
h quality sequence stop: 449.
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'tissue_type="embryo"
'dev_stage="13.5-14.5dpc total fetus"
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'clone="IMAGE:403452"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                          10.3%;
                                                        504 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 g
                                                          mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                          DB 27;
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                                                                                                                            RESULT 11
AI785404/c
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Best Local
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                                                                                                                                                                                                                                                                                                   158 ACCACTTAAGCAGCTGGTTGACAGACGCA 186
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                                                                                                                                                                                                                                                                                                                                              gcgatctaagcggcgagaccggagacgca 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAAACTGCAGATTTGGGATACAGCAGGGCAGGAGCGGTTCAGAGCGGTTACACGGAGCT 97
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Eutharyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 504)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Thetasing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HHMI Mouse EST Project
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On Apr 18, 1995 this sequence version replaced g1:775526.
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
AI785404 513 bp mRNA EST 02-JUL-1999 uj41e10.xl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1922538 3' similar to SW:RB14_RAT P35287 RAS-RELATED PROTEIN
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Similarity 52.3%;
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/lab_host="D
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1263414"
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/sex="male"
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Pred. No. 0.76;
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                                                                                                                                        135 cgaagccaggggggcgcctggatgctttgagagagtggatatactactactactactactacacaga 194
                                                                                                                                                                                                  359 TCAGACTGCAGATTTGGGATACAGCAGGGCAGGAGCGGTTCAGAGCGGTTACACGGAGCT 300
  239
                                                                                                 299 ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA 240
                                                                                                                                                                                                                                         75 ttattctgcggtggtggatgttatcagggcagcggcgcatgaaggagtttacatagaacc 134
                                                                                                                                                                                                                                                                                                                           Local
  ACCACTTAAGCAGCTGGTTGACAGACGCA 211
                                          gcgatctaagcggcgagaccggagacgca 223
                                                                                                                                                                                                                                                                                           10.3%;
1 Similarity 52.3%;
78; Conservation
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The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on Jun 22, 1998 this sequence version replaced gi:3247490. Contact: Marra M.WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI785404
AI785404.1 GI:5333120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: custom primer used High quality sequence stop: 451.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
TMACE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         140
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-*Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG] digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."

40 a 122 c 86 g 165 t
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/clone_lib="Sugano mouse kidney mkia"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                           Score 35.4; DB Pred. No. 0.77;
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                                                                                                                        512
                                                                                                                                                                                                                                                 452 ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA 511
                                                                                                                                                                                                                                                                                                                   135 cgaagccaggggggcgcctggatgctttgagagagtggatatactacaactactacacaga 194
                                                                                                                                                             195 gcgatctaagcggcgagaccggagacgca 223
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                                                                                                                     ACCACTTAAGCAGCTGGTTGACAGACGCA 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.3%;
1 Similarity 52.3%;
78; Conservation
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17'(bases 1 to 543)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wile, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMI Mouse EST Project
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On Sep 12, 1996 this sequence version replaced gi:14071
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Barkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further j
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Location/Qualifiers
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AA140104
AA140104.1 GI:1702468
EST.
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/tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SoLR (Kanamyoin resistant)"
/lab_host="SoLR (Kanamyoin resistant)"
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Vector: pBluescript Street: Note: pBluescript Street: pBluescript Street: Note: pBluescript Street: Note: pBluescript Street: Note: pBluescript Street: Note: pBluescript Street: pBluescript Street: Note: pBluescript Street: pBluescript Street: Note: pBluescript Street: Note: pBluescript Street: pBluesc
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/strain="NIH/Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:586256"
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Pred. No. 0.79;
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Matches 78
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195 gcgatctaagcggcgagaccggagacgca 223
                                                                                                                                                                     75 ttattctgcggtggtggatgttatcagggcagcggcgcatgaaggagtttacatagaacc 134
                                               ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAAAAGAAGTACATATA
                                                                                         cgaagccagggggcgcctggatgctttgagagagtggatatactacaactactacacaga 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1393035.
Contact: Marra Myouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 547)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
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                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="IMAGE:790334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="Barstead MPLRB1"
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                                                                                                                                                                                                                                Score 35.4; DB 31;
Pred. No. 0.79;
0; Mismatches 71;
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                                                                                                                                                                                                                                                                          Length 547;
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BASE COUNT
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AUTHORS
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                                     135 cgaagccagggggggcctggatgctttgagagagtggatatactacaactactacacaga 194
                                                                                    62
                                                                                                       ttattctgcggtggtggatgttatcagggcagcggcgcatgaaggagtttacatagaacc 134
ACTATAGAGGAGCTGCAGGTGCGCTCATGGTGTATGACATCACCAGAAGAAGTACATATA 282
                                                                               TCAAACTGCAGATTTGGGATACAGCAGGGCAGGAGCGGTTCAGAGCGGTTACACGGAGCT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI784945 551 bp mRNA EST 02-JUL-1999 uj22a03.x1 Sugano mouse kidney mkia Mus musculus CDNA clone IMAGE:1920652 3' similar to SW:RB14_RAT P35287 RAS-RELATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jun 22, 1998 this sequence version replaced gi:3247058. Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 551)
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AI784945.1 GI:5332696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                ;, mRNA sequence.
                                                                                                                                                                                                                                                                                             Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

123 c 92 g 186 t
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/db_xref="taxon:10090"
/clone="IMAGE:1920652"
/clone_lih="Sugano mouse kidney mkia"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism-"Mus musculus"
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                                                                                                                                                                                     10.3%;
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                                                                                                                                                                 Score 35.4; DB 60;
Pred. No. 0.79;
0; Mismatches 71;
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Query Match Best Local (Matches 78

Similarity

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DB 43;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
On Jan 19, 1998 this sequence version repl
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI195511 556 bp mRNA EST 14-OCT-1 1M30g10.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1885890 5' similar to SW:RB14_RAT P35287 RAS-RELATED
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, Geisel, S., Kucaba, T., Lacy, M., Le, M., Marrin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: custom primer used High quality sequence stop: 509 Location/Qualifiers
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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     [ATGTGGCCTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTTTGCTTCTAAAAGCTTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                           138
                                                                                                                                                                                                                                                                                                           /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDN.
was primed with an oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Mus musculus"
/strain-"C57BL"
/db_xref-"taxon:10090"
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	pDE4; pl Plasmid Plasmid Sequence	PATI ge pTrc 99 PATI ge pUMIGIT	Tobacco o Sequence Polynucle Sequence	Human m Human m	Adenovirus 17.	Chimeri	Plasmid	Chimpanzee Chimpanzee	Adenovirus	Adenovirus 5	Recombinant	Recombinant Adenoviral	Complete	Adenovirus	Descriptio		e to have t being poution.			÷	23170			cgtacag	56.99 Seconds alignments) Million cell updates/se		
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	cgcTccT	0%; Sc 0%; Pr	ibrosis rs, vir	95 and 1 nts 3 1 erated	s all c	Tregic	ch is i	region	ecombin	the ad	n of th	espondi Ad5) k	9pp; Fr	E1 and	binant	ni C,	ER SA		; blood	d tande	Rregio	89 BP.			1 V61792 1 V61793 1 V61794 1 V61794		
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15/c 131315; standard; cl 131315; 16-APR-1997 (firs Adenovirus E4 and] Human adenovirus A5 20-JAN-1995; FR-00) 01-JUN-1995; FR-00] 01-JUN-195; FR-00] 01-JUN-195; FR-00] 01-JUN-195; FR-00] 01-JUN-195; FR-00	28 29 29 29 29 29 29
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standard; cDNA; 3189 BP. 12-1997 (first entry) 12-1997 (first entry) 13-1997 (first entry) 13-1996; end line 13-1996; end line 13-1996; end line 13-1997; end lisease; blood 13-1997; end lisease; 1-1997; end lisease; lisease 1-1997; end lisease 1-1997; end lisease; lisease 1-1997; end lisea	7742 9299 9335 9408 10160 11198 11991 14698 19001 19035
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T31315; standard; cDNA; 3189 BP. T31315; standard; cDNA; standard; cdefective recombine complementation; gene therapy; cystic fibrosis; dystineurodegenerative disease; blood coagulation disorder Adenovirus AdS. T20-TAN-1995; FR-000747. T20-TAN-1995; FR-000532. T20-T	V03430 V63734 V63734 V63731 V63723 V63724 V63725 V61792 V61793 V61794 Q03098 ALIGNMENTS
T33115 standard; cDNA; 3189 BP. T331215, standard; cDNA; 3189 BP. T331315, standard; cDNA; 3189 BP. T331315, standard; cDNA; 3189 BP. Adenovirus 44 and part ITR region corresp. to bases 32749-35935. Adenovirus 54 and part ITR region corresp. to bases 32749-35935. Adenovirus 45. Adenovirus 45. Adenovirus 45. Adenovirus 45. Adenovirus 45. Adenovirus 45. Adenovirus 45. Adenovirus 45. Adenovirus 46. Adenovirus 57. Adenovirus 47. 101-JPM-1995; FR-000547. 101-JPM-1995; FR-	Escherichia coli g Vector plasmid Per Plasmid PIGP/367 c Vector plasmid PER Vector plasmid pDA Vector plasmid pDA Vector plasmid pDA Traget plasmid Mol Traget plasmid Mol Enod2a genomic clo

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cc method of the invention. The plasmid contains an adenovirus type 5 ct 4 regulatory gene and a hygromycin resistant gene. The invention cc provides adenoviral vectors having deletions of all or part of correct or various gene sequences encoding adenoviral structural proteins. Cc Deletions in the structural proteins would allow a reduced risk of cwild-type virus contamination and would also allow packaging of foreign cc DNA in such vectors for a variety of diagnostic and therapeutic camplications. The adenoviral vectors having deletions in the structural gene regions are produced by cellular complementation of these complementation plasmid which was introduced into a sa complementation plasmid which was introduced into a host cell line where parts of the E4 gene region would be stably inserted into the cc where parts of the E4 gene region would be stably inserted into the cc where parts of the E4 gene region would be stably inserted into the cc as a gene delivery vector. The vectors can be used for diagnosis or gene therapy, e.g. for treating conditions characterised by the crown of the call (e.g. tumours), genetic diseases (e.g. through the conditions characterised by cromitations (e.g. HIV infection). They can also be used for in vitro cc production of biologically active proteins.
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                                                                                                                                                                                                                                                                                                                                                                                         or fibre protein used particularly for gene therapy Example 1; Pages 63-74 170pp; English.

The present sequence is that of a pE4/Hygro plasmid used in the method of the invention. The plasmid contains an adenovirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete sequence of the pE4/Hygro plasmid.
Circular; adenovirus type 5; pE4/Hygro plasmid; structural protein;
complementation; E4 regulatory protein; gene therapy; HIV; tumour;
Huntington's disease; Tay-Sachs disease; sickle cell disease;
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(SCRI ) SCRIPPS RES INST.
Memerow GR, Von Seggern DJ;
WPI; 98-230709/20.
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24-SEP-1997; E05251.
25-SEP-1996; US-719806.
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V32370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                denoviral vectors - which lack DNA encoding for structural protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "E4 regulatory gene" 3830. .6470
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PA (NOVS) NOVARTIS AG:

PA (NOVS) NOVARTIS RES INST.

PI Memerow GR, Von Seggern DJ;

PT or fibre protein used particularly for gene therapy

PS Example 1; Pages 131-145; 170pp; English.

CC The present sequence is that of a pE4/Fiber plasmid used in the

CC method of the invention. The plasmid contains an adenovirus type 5 (AD5)

CC fiber gene controlled by a CMV promter, an AD5 E4 gene and an adenovirus

CC type 2 (AD2) tripartite leader sequence upstream of the fiber gene. The

CC various gene sequences encoding adenoviral structural proteins and/or

CC various gene sequences encoding adenoviral structural proteins and/or

CC early region proteins. Deletions in these proteins would allow a

CC reduced risk of wild-type virus contamination and would also allow

CC packaging of foreign DNA in such vectors having deletions in
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Best Local
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24-SEP-1997; E05251.
25-SEP-1996; US-719806.
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sickle cell
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 therapeutic applications. The adenoviral the structural and/or early gene regions
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345; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA; 10610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease; E4 regulatory gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "AD5 E4 regulatory gene"
4051. .4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (21. .3149)
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "AD5 leader sequence"
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The adenoviral vectors having deletions in y gene regions are produced by cellular
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Pred. No. 8.2e-105;
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AD5;
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EDb 1411 ACGACCAACACGATCTCGGTTGTCTCGGCGCACTCCGTACAGTAG 1367
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complementation of these adenoviral genes. Therefore, the pE4/Fiber plasmid was used as a complementation plasmid which was introduced into a host cell line where parts of the fiber and E4 gene region would be stably inserted into the host cell chromosomes. The resulting E4/fiber gene deficient plasmid can be used as a gene delivery vector. The vectors can be used for diagnosis or gene therapy, e.g. for treating conditions characterised by hyper-proliferative cells (e.g. tumours), genetic diseases (e.g. Huntington's disease, Tay-Sachs disease, or sickle cell disease), or infections (e.g. HIV infection). They can also be used for in vitro production of biologically active proteins. Sequence 10610 BP; 2807 A; 2821 C; 2446 G; 2536 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - 1
Chimeric - 1
and durable transgene expression

Example 2; Fig 10A-H; 74pp; English.

This is the DNA sequence of the recombinant adenovirus

H5.020TKneo-int. It was obtained by co-transfecting HEK293 (ATCC CRL1573) cells with linearised plasmid padneo-int (see T6055) and Ad5d17001. It was used as a control in studies of the retrotransposition and integration of cis- and trans-acting recombinant adenoviruses (see T60557 and T60558) into host cells. Claimed novel recombinant replication defective viruses (A) comprise: (a) DNA of, or corresponding to, at least part of the viral genome, able to infect a mammalian cell; and (b) a first
                                                                                                                                                                                                                                     01-MAY-1997.
24-OCT-1996; U17176.
27-OCT-1995; US-005942.
(UYPE-) UNIV PENNSYLVANIA.
Relley WM, Wilson JM;
WPI; 97-259031/23.
Recombinant replication defective virus - inserts transgene into host cell chromatin in the presence of transposase, providing stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1651
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Recombinant adenovirus H5.020TKneo-int.

Adenovirus H5.020TKneo-int; plasmid pAdMLVneo-int; Ad5; Mo-MLV;

retrovirus retrotransposition; transposition; transgene;

gene therapy; vector; neomycin resistance; neo gene; ss.

Chimeric - Mastadenovirus serotype 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,1531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T60559 standard; DNA; 32026
T60559;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aactactacacagagcgatctaagcggcgagaccggagacgcagatctgtttgtcacgcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | atggttcttccagctcttcccgctcctcccgtgtgtgactcgcagaacgaatgtgtaggt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PACTACTACACAGAGCGATCTAAGCGGCGAGACCGGAGACGCAGATCTGTTTGTCACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGCTGGGTGTGCCTTATTCTGCGGTGGTGGATGTTATCAGGGCAGCGGCGCCATGAAGGA 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tggctgggtgtggcttattctgcggtggtggtgttatcagggcagcggcgcgcatgaagga 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTTACATAGAACCCGAAGCCAGGGGGCGCCTGGATGCTTTGAGAGAGTGGATATACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 345; DB 1;
Pred. No. 8.9e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    flanked by DNA of (a); (A) can infect a mammalian cell and ESI
c flanked by DNA of (a); (A) can infect a mammalian cell and can
c express (I) and transfer it to the cellular chromatin in vivo or in
c vitro in the presence of a transposase. Also new are: (1) a
recombinant replication defective virus (B) containing (a) as above
and a second expression sequence (ES2) containing a trans-acting
transposase gene (II) plus regulatory sequences, flanked by DNA of
(a) and able to express transposase in mammalian cells; and (2)
mammalian cells which stably express (I) integrated into its
chromatin, produced by infection with (A). (A) and (B) are used
for delivery and stable integration of (I) into a host cell
(claimed), e.g. in somatic gene therapy of genetic defects or
deficiencies such as cystic fibrosis. (A) are also used to prepare
recombinant retroviruses (RRY) (claimed). Because (I) becomes
stably integrated, it provides longer lasting expression than genes
introduced with conventional adenoviral vectors and the need for
repeated administration is avoided. The transgene is inherited by
the
progeny cells and the viral component is gradually degraded by the
cell. When used for RRV production, (A) increase the ratio of RRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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                                                                                                                                                                                          28-SEP-1998 (first entry)
Adenoviral vector plasmid pBHG11.
Adenovirus 5; Ad5; vector; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression sequence (ES1) comprising a human regulatory sequences for expression, with the cis-acting terminal repeat sequences of a
                                                                                                                                                                    Key
                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                      V07261 standard; DNA; 34303
V07261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to empty retrovirus. Sequence 32026 BP;
                                                                                                                                                                                   Mastadenovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGACCAACACGATCTCGGTTGTCTCGGCGCACTCCGTACAGTAG
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                                                                                                                                                                                                                                                                                                                                                                         acgaccaacacgatctcggttgtctcggcgcactccgtacagtag
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                                                                                                                                                                                                                                                                                                                                                                                                                                        cgcacctggttttgcttcaggaaatatgactacgtccggcgttccattttggcatgacact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGTTCTTCCAGCTCTTCCCGGTCCCCGTGTGTGACTCGCAGAACGAATGTGTAGGT 30374
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                                                                                  8773.
                                                                                                                                               Location/Qualifiers'
8772. 9385
                                                                                100.0%;
"region deleted in plasmid paxBdelpoldelpTPVARNA+t13 and pBHG11delpolydelpTPVARNA+t13 .11134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 345; DB 1;
Pred. No. 1.4e-104;
); Mismatches 0;
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                                                                                                               pdepTP
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               (Claim
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on, and ES1
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misc_feature

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This nucleotide sequence comprises plasmid pBHG11 that consists of 2C an E1-deleted adenovirus (Ad) genome. It contains a deletion of 2C an E1-deleted adenovirus (Ad) genome. It contains a deletion of 2C and5 (see also V0728) from bp 188-1339 (0.5-3.7 m.u.). This 2C deletion removes the packaging signals as well as E1 sequences. CC pBHG11 also contains a large deletion within the E3 region (bp 2C 27865-30995, 77.5-86.2 m.u.). Nucleotide 8773 of pBHG11 is 2C equivalent to nucleotide 7269 of Ad5. The large E3 deletion 2C provides a large cloning capacity to Ad vectors based on pBHG11. CC Recombinant plasmids pdelpol and pBHG11delpol (deleted for E1 and 2C polymerase functions), and pAXBdelpoldelpyTyARNA+13 and 2C perterminal protein functions), are specifically claimed. The 2C invention provides improved adenoviral vectors and packaging 2C within the E2D region of the adenoviral vectors and packaging 2C within the E2D region of the adenoviral genome (see also V07261). CC These E2D-deleted virus are used in conjunction with novel cell 2C witted vectors deleted for all viral coding regions. These 2CC salted vectors deleted for all viral coding regions. These 2CC salted vectors and sectors deleted for all viral coding regions. These 2CC witted vectors and sectors deleted by the transfer of the dystrophin 2CC signer to the muscle of mice. The E2D-deleted and gutted vectors convolde improved adenoviral vectors useful for a wide variety of
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 345; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example to the muscle of mice. The E2b-delete approvide improved adenoviral vectors useful gene therapy applications.

Tisequence 34303 BP; 7948 A; 9625 C;
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Amalfitano A, Chamberlain JS,
Hauser MA, Kumar-Singhr;
WPI; 98-261485/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New adenoviral recombinant plasmid(s) for expression of large foreign DNA f. therapy of genetic disease(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                  181
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                                                                                                                                                                                                                                                                                                                                                     acgaccaacacgatctcggttgtctcggcgcactccgtacagtag
                                                                      cgcacctggtttttgcttcaggaaatatgactacgtccggcgttccatttggcatgacact
                                                                                                                                                 aactactacacagagcgatctaagcggcgagaccggagacgcagatctgtttgtcacgcc
                                                   CGCACCTGGTTTTGCTTCAGGAAATATGACTACGTCCGGCGTTCCATTTGGCATGACACT
                                                                                                                             AACTACTACACAGAGCGATCTAAGCGGCGAGACCGCAGATCTGTTTGTCACGCC
                                                                                                                                                                                                      gtttacatagaacccgaagccagggggcgcctggatgctttgagagagtggatatactac
                                                                                                                                                                                                                                                                              TGGCTGGGTGTGGCTTATTCTGCGGTGGTGGATGTTATCAGGGCAGCGGCGCATGAAGGA
                                                                                                                                                                                                                                                                                                    tggctgggtgtggcttattctgcggttggtggatgttatcagggcagcggcgcatgaagga 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 345; DB 1; 100.0%; Pred. No. 1.4e-104; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "region deleted in plasmid
pAXBdelpoldelpTPVARNA+t13 and
pBHG11delpolydelpTPVARNA+t13 (Claim 53)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region deleted in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   рвиG11delpTP
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(Claim 51)"

    comprise sequences provided
ragments, used for, e.g. gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 34303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proposed the Ela and Ela regions - containing a single packaging signal sequence and proposed the sequence represents recombinant adenovirus proposed the present sequence represents recombinant adenovirus and sequence contains and comprises a single packaging signal sequence contains and the Ela and Ela regions and comprises a single packaging signal sequence contains and the Ela deletion contains at least one paci, Clai, Xbal corrections and the Ela deletion contains at least one paci, Clai, Xbal corrections and the Ela deletion contains at least one paci, Clai, Xbal corrections of the state of sequence site. The replication deficient viral vectors can be used in gene therapy regimens to effect the transfer of genes encoding conclude synthetase (NOS) gene (brain, endothelial and microphage NOS), the conclude synthetase (NOS) gene (brain, endothelial and microphage NOS), the conclude synthetase (NOS) gene (brain) gene. The NOS isoforms can be concluded into vein grafts prior to their use as compared to the sequence of the sequence o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Blazing MA, George SE;
WPI; 99-204005/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant adenovirus Ad:Pac-beta-Gal.
Recombinant adenovirus Ad:Pac-beta-Gal; replication deficient adenovirus;
Recombinant adenovirus Ad:Pac-beta-Gal; replication deficient adenovirus;
Ela region; E3 region; gene therapy; nitric oxide synthetase; NOS;
cystic fibrosis chloride channel; LDL receptor; erythropoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27/c
X15627
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74387 RP: 7923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atherosclerotic artery; ss.
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07-мау-1999
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17-JAN-1995;
                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%;
Local Similarity 100.0%;
tes 345; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                 aactactacacagagcgatctaagcggcgagaccggagacgcagatctgtttgtcacgcc
                                                                                                                                                                                                                           gtttacatagaacccgaagccaggggggcgcctggatgctttgagagagtggatatactac
       CGCACCIGGITTIGCITCAGGAAATAIGACIACGICCGGCGITCCAITIGGCAIGACACI
                                  cgcacctggttttgcttcaggaaatatgactacgtccggcgttccatttggcatgacact
                                                                                                                                                                                                  GTTTACATAGAACCCGAAGCCAGGGGGGCGCCTGGATGCTTTGAGAGAGTGGATATACTAC
                                                                                                                                                                                                                                                                                              TGGCTGGGTGTGGCTTATTCTGCGGTGGTGGATGTTATCAGGGCAGCGGCGCATGAAGGA
                                                                                                                                                                                                                                                                                                                    tggctgggtgtggcttattctgcggtggtggatgttatcagggcagcgggggcgcatgaagga 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 345; DB 1;
Pred. No. 1.4e-10;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9880 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9421 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 34382;
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32244
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Db 32243 ACGACCAACACGATCTCGGTTGTCTCGGCGCACTCCGTACAGTAG
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                                                                                                                                                                                                                                                              Principle of the presence of transposase, providing stable principle and durable transgene expression

Example 2; Fig 8A-1; 74pp; English.

CThis is the DNA sequence of the cis-acting recombinant adenovirus CC His 1s the DNA sequence of the cis-acting recombinant adenovirus CC (ATCC CRL1573) cells with linearised plasmid pAdMLYneo-int (18e 760554) and Ad5617001. A trans-acting adenovirus (see CC F00558) was also produced, and retrottansposition and integration CC viruses. Claimed novel recombinant replication defective viruses (A) comprise: (A) DNA of, or corresponding to, at least part of the CC viruses. Claimed novel recombinant replication defective viruses (C) the cis-acting terminal repeat sequences of a transposon, and ESI CC expression sequence (ESI) comprising a human gene (I) linked to regulatory sequences for expression, with the cassette flanked by the cis-acting terminal repeat sequences of a transposon, and ESI CC express (I) and transfer it to the cellular chromatin vivo or in CC transposase sequence (II) plus regulatory sequences, flanked by DNA of (a); (A) can infect a mammalian cell; and (2) are combinant replication defective virus (B) containing (a) as above and a second expression sequence (ES2) containing a trans-acting CC virusesposase gene (II) plus regulatory sequences, flanked by DNA of (a) and able to express transposase (I) integrated into its mammalian cells which stably express (I) integrated into its chromatin, produced by infection with (A). (A) are also used to prepare (C claimed), e.g. in somatic gene therapy of genetic defects or deficiencies such as cystic fibrosis. (A) are also used to prepare (C claimed) integrated, it provides longer lasting expression than genes culturoduced with convention is avoided. The transgene is inherited by the correspondence of a ransolded. The transgene is inherited by the correspondence of a containing a crans cell containing a
                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-OCT-1996; U17176.
27-OCT-1995; US-005942.
(UTPE-) UNIV PENNSYLVANIA.
Kelley WM, W11son JM;
WPI; 97-259031/23.
                                              33407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant cis-acting adenovirus H5.020Tkneo-int(LTR). Adenovirus H5.020Tkneo(LTR); plasmid pAdMLvneo-int; retrovirus; retrotransposition; transposition; transgengene therapy; vector; neomycin resistance; neo gene; ss Chimeric - Mastadenovirus serotype 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T60557 standard; DNA; 35000 T60557;
                                                                                                                                                                                                                                                            to empty retrovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAR-1998 (first entry)
      ដ
                                                                                                                                                    Local
                                          atggttcttccagctcttcccgctcctcccgtgtgtgactcgcagaacgaatgtgtaggt 60
tggctgggtgtggcttattctgcggtggtggatgttatcagggcagcggcatgaagga 120
                                                                                                                                al Similarity
345; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus sp. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moloney murine leukaemia virus
                                                                                                                            100.0%;
Llarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                      7810 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                              0
                                                                                                                            Score 345; DB 1;
Pred. No. 1.4e-104;
Mismatches 0;
                                                                                                                                                                                                                                      9673 C;
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                                                                                                                                                                   Length 35000;
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181 aactactacacagagcgatctaagcggcgagaccggagacggcagatctgtttgtcacgcc

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                                                                                                                                                                                                                                             New adenoviral recombinant plasmid(s) - comprise sequences provided for expression of large foreign DNA fragments, used for, e.g. gene therapy of genetic disease(s) bisclosure; Page 69-86; 139pp; English.

This nucleotide sequence comprises the adenovirus 5 (Ad5) genome. The invention provides improved adenoviral vectors and packaging cell lines. One type of improved vector comprises deletions within the E2b region of the adenoviral genome (see also v07261).

These E2b-deleted virus are used in conjunction with novel cell lines that constitutively express E2b gene products. The invention calso provides vectors deleted for all viral coding regions. These 'gutted' vectors permit the transfer of large genes (e.g. up to 25 kb) to cells, as demonstrated by the transfer of the dystrophin gene to the muscle of mice. The E2b-deleted and gutted vectors gene to the muscle of mice. The E2b-deleted and gutted vectors gene therapy applications.

So Sequence 35935 BP; 8367 A; 10074 C; 9760 G; 7734 T;
                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                           Query Match
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30-APR-1998.
23-OCT-1997; U19541.
23-OCT-1996; US-735609.
(UNMI) UNIV MICHIGAN.
Amalfitano A, Chamberlain J;
Hauser MA, Kumar-Singhr;
WPI; 98-26185/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mastadenovirus 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adenovirus 5; Ad5; vector; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V07258
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                             121
                                                                                       61
                                                                                                                                                                             Local Similarity
les 345; Conserv
                                                        TGGCTGGGTGTGGCTTATTCTGCGGTGGTGGATGTTATCAGGGCAGCGGCGCATGAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tggctgggtgtggcttattctgcggtggtggatgttatcagggcagcggggggcatgaagga 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acgaccaacacgatctcggttgtctcggcgcactccgtacagtag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cgcacctggttttgcttcaggaaatatgactacgtccggcgttccatttggcatgacact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTTACATAGAACCCGAAGCCAGGGGGGCGCCTGGATGCTTTGAGAGAGTGGATATACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGACCAACACGATCTCGGTTGTCTCGGCGCACTCCGTACAGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCACCTGGTTTTGCTTCAGGAAATATGACTACGTCCGGCGTTCCATTTGGCATGACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTTACATAGAACCCGAAGCCAGGGGGGGCGCCTGGATGCTTTGAGAGAGTGGATATACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA; 35935
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS, Hartigan-OConnor DJ
                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВР
                                                                                                                                                                            Score 345; DB 1;
Pred. No. 1.5e-104;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy;
                                                                                                                                                                                                        Length 35935;
                                                                                                                                                                             Indels
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                                                                                                                                                                                                                       calso produced, and retrotransposition and integration into host cells was demonstrated in HeLa cells infected with both viruses. Claimed novel recombinant replication defective viruses (A) comprise: (A) DNA of, or corresponding to, at least part of the comprise: (B) DNA of, or corresponding to, at least part of the creative viruses (F) and the cell; and (C) a first expression sequence (ESI) comprising a human gene (I) linked to regulatory sequences for expression, with the cassette flanked by the cis-acting terminal repeat sequences of a transposon, and ESI clanked by DNA of (a); (A) can infect a mammalian cell and can express (I) and transfer it to the cellular chromatin in vivo or in vitro in the presence of a transposase. Also new are: (I) a recombinant replication defective virus (B) containing (a) as above and a second expression sequence (ES2) containing a trans-acting transposase gene (II) plus regulatory sequences, flanked by DNA of (a) and able to express transposase in mammalian cells; and (2) cmammalian cells which stably express (I) integrated into its chromatin, produced by infection with (A). (A) and (B) are used for delivery and stable integration of (I) into a host cell (claimed), e.g. in somatic gene therapy of genetic defects or deficiencies such as cystic fibrosis. (A) are also used to prepare recombinant retroviruses (RW) (claimed). Because (I) becomes stably integrated, it provides longer lasting expression than genes introduced with conventional adenoviral vectors and the need for concepted administration is availed.
    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and durable transgene expression

Example 2; F1g 9A-1; 74pp; English.

This is the DNA sequence of the trans-acting recombinant adenovi:

H5.020CMYgag-pol. It was obtained by co-transfecting HEK293

(ATCC CRL1573) cells with linearised plasmid pAdCMYgag-pol (see
T60555) and Ad5d17001. A cis-acting adenovirus (see T60557) was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-1996; U17176.
27-OCT-1995; US-005942.
(UYPE-) UNIV PENNSYLVANIA.
Kelley WM, Wilson JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant trans-acting adenovirus H5.020CMVgag-pol. Adenovirus H5.020CMVgag-pol; plasmid pAdMLVneo-int; Ad5; retrovirus; retrotransposition; transposition; transposition;
                                                                                                                                        g
                                                                                                                                                        repeated administration is avoided. The transgene is inherited by progeny cells and the viral component is gradually degraded by the cell. When used for RRV production, (A) increase the ratio of RRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant replication defective virus - inserts transgene into host cell chromatin in the presence of transposase, providing stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric - Cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Mastadenovirus serotype 5.
Chimeric - Moloney murine leukaemia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; vector; ss.
Chimeric - Mastadenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T60558 standard; DNA; 36538
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Local Similarity
les 345; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cgcacctggttttgcttcaggaaatatgactacgtccggcgttccatttggcatgacact 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97-259031/23.
                                                                                                             When used for RR
ty retrovirus. •
ce 36538 BP;
                       100.0%;
                                                                                                                  8621 A;
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  0;
Score 345; DB 1;
Pred. No. 1.5e-104;
; Mismatches 0;
                                                                                                                10490 C;
                                                                                                                  9909 G;
                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33998
                                               36538;
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                                                                                                                  7518 T;
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Gaps
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Example 10; Fig 28A-XX; 126pp; English.

CC This is the nucleotide sequence of vector 231-10, a human cadenovirus serotype 5 (Ad5) vector. 231-10 lacks the EIA, EIB cc adenovirus serotype 5 (Ad5) vector. 231-10 lacks the EIA, EIB cc adenovirus serotype 5 (Ad5) vector. 231-10 lacks the EIA, EIB cc adenovirus serotype 5 (Ad5) vector. 231-10 lacks the EIA, EIB cc adenovirus serotypes 5 (Ad5) vector. 231-10 lacks the EIA regions are cc and EIB transcription units. The deleted EIA and EIB regions are created and EIB regions are created and EIB regions are created with an expression cassette wherein all the EI proteins. The care expression of the human cytomegalovirus (CMV) promoter. The CC aderivative of virus rec700, which is an Ad5-Ad2-Ad recombinant ct that has the Ad2 version of the EI genes for the 12.5%, 6.7%, cc gplsk and RID-bata and 14.7% proteins. In addition, the vector has cc missense mutations in the adp (adenovirus death protein) genes cf that eliminate the first 2 Met codons, thereby precluding synthesis cof functional ADP. Because 231-10 lacks EIA, viral genes in the created by containing the vector serves as an cc expressed from the CMV promoter. Thus, the vector serves as an cc essentially inert vehicle by which EI genes can be delivered into cc cells. The invention provides a method for inhibiting apoptosis of CC a cell expressing a death receptor of the tumour necrosis factor internalisation and degradation (RID) protein complex containing cc expressing the RID complex or a composition containing the RID complex. The complex or a composition containing the RID complex. The complex or a composition containing the RID complex. The compositions and methods are used to treat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Mastadenovirus 5.
Chimeric - Mastadenovirus 2.
Chimeric - Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adenovirus vector 231-10 genome.
Adenovirus; vector 231-10; apoptosis; inhibitor; RID-alpha;
RID-beta; receptor internalisation and degradation; cancer;
degenerative disease; immune disorder; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUL-1998;
09-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9902658-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue transplant; death receptor; tumour human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             degradation (RID) complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Method for inhibiting apoptosis - using receptor internalisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wold WSM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
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Best Local Similarity
Matches 344; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-AUG-1998 (first entry)
Chimpanzee adenovirus C68 genomic sequence.
genomic sequence; virus gene therapy; treat
genomic defects; inherited defects; genetic engineering;
an vitro production; recombinant protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the cells.
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10823.
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/note= "E1B gene"
complement(23370.
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1560. .3956
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complement(10346.
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Pred. No. 4.9e-104;
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Best Local Similarity
Matches 217; Conserv
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04-SEP-1997; U15694.

06-SEP-1996; US-024700.

(UYPE-) UNIV PENNSYLVANIA.

Farina SF, Fisher KJ, Wilson JJ

WPI; 98-193635/17.
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The sequence is that of the chimpanzee adenovirus C68. It mands to sequence is that of the comprising it and a select used in the production of a vector comprising it and a select heterologous gene operatively linked to regulatory sequences directing its expression in a heterologous cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Such recombinant adenoviruses are useful as vectors in gene therapy and genetic engineering in general, especially for the treatment of aquired or genetically inherited defects. The viruses are also useful for the in vitro production of recombinant proteins of interest.

Sequence 36519 BP; 7809 A; 10790 C; 10623 G;
          Chimpanzee adenovirus Cl genomic sequence. genomic sequence; virus; gene therapy; treatment; genomic sequence; virus gene therapy; treatment; acquired defects; inherited defects; genetic engineering; vecto in vitro production; recombinant protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimpanzee adenovirus vector - useful in
                                                                       17-AUG-1998
                                                                                                  V22140 standard;
                                                                                                                                                                                                                                                                                                                                                                                 121
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/note=
17480.
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32134.
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.33502
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Pred. No. 1e-37;
0; Mismatches 122;
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a selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36519;
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Best Local Similarity 60.6%;
Matches 169; Conservative
                                                                                                                                                                                                                         Query Match
                                                                                                                                             33994
                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1998.
04-SEP-1997; U15694.
06-SEP-1996; US-024700.
(UYPE-) UNIV PENNSYLVANIA.
Farina SF, Fisher KJ, Wilson JJ
WPI; 98-193635/17.
                                  33874
                                                                                       33934
                                                                                                                                                                                                                                                                                                   theterologous gene operatively linked to regulatory sequences directing its expression in a heterologous cell. Such recombinant adenoviruses are useful as vectors in gene therapy and genetic engineering in general, especially for the treatment of aquired or genetically inherited defects.
                                                                                                                                                                                                                                                           the treatment of aquired or genetically inherited defects. The viruses are also useful for the in vitro production of recombinant proteins of interest.

Sequence 35524 BP; 8873 A; 9142 C; 9033 G; 8
                                                                                                                                                                                                                                                                                                                                                                    engineering in general
Disclosure; Pages 51-70; 116pp; English.
The sequence is that of the chimpanzee adenovirus C1.
used in the production of a vector comprising it and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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CDS
                                                                                                                                                                                                                                                                                                                                                                                                                         Chimpanzee adenovirus vector - useful in gene therapy and genetic
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                                                                                  TGGTTGGGTATTGCCCCATTCTACAGTGAATGATTTTATCAGAGCGATCAGACATGATGGA 33875
                                                                                                                                      aactactacacagagcgatctaagcggcgagaccggagacgcagatctgtttgtcacgcc 240
                                GTTTTCATAACAACTGAAGCCGAGGAACTTTTGACCAATCTACGGGAATGGCTGTACTTC
                                                gtttacatagaacccgaagccagggggcgcctggatgctttgagagagtggatatactac 180
                                                                                                 tggctgggtgtggcttattctgcggtggtggttgttatcagggcagcggcggcatgaagga 120
                                                                                                                                                      atggttcttccagctcttcccgctcccgtgtgtgtgactcgcagaacgaatgtgtaggt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "E2A gene"
omplement(10379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note- "E3 gene"
omplement(35228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note- "ElB gene"
omplement(23665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          = "ElA gene" .3958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "E2B gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "L2 gene"
.22083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "L4 gene"
.32551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "E4 gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "L5 gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .13864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "L3 gene"
.27813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L1 gene"
                                                                                                                                                                                            Score 103; DB 1;
Pred. No. 3.6e-24;
0; Mismatches 110
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                                           cds
                                                                                              cds
                                                                                                                                                                                                                                                 cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
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                                                                                                                                    polya_signal
                                                                                                                                                                                            cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                     cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant adenovirus; Ad2/CFTR-1; adenovirus 2 serotype; Ela; Elb; viral replication; gene expression; gene therapy; cystic fibrosis; cystic fibrosis transmembrane conductance regulator; CFTR; promoter; E3; p19; MHC; class 1; viral latency; pulmonary airway; ds
                                                                                                                                                                                                                                                                                                                                         polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-1996 (first entry)
Ad2/-ORF6/PGK-CFTR nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           068003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268003 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
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                                                                                              /note-
20240.
                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12915.
                                                                   'product= pVI
                                                                                                                                                  note-
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12915. .36335
                                                                                                                                                                                                                    product= Pro-VII
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                                                                                                                                                                                                                                             product= Penton protein note= "virion component 3112. .18708
                                                                                                                                                                                                                                                                                                                                                                                             luct= 52,55K protein . .16304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36335
                                        "Hexon . 23983
                                                                                                                                                                                         "Precursor .19887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 29366
                                                                                                                                                                                                                                                                                                                                                                                                                                               "33K protein"
                                                                                             "major
.20992
                                                                                                                                                                                                                                                                                                                                                   "Peripentonal hexon-associated protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .28992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Represents residues 10676-34096 of Ad2-E4/ORF6" .35973
                                                                                                                                      20193
                                                                                                                                                                                                                                                                                                  Major late mRNA L1 poly A signal (putative)" 18105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Represents residues 33178-34082 of Ad27 35054
                                                                                                                                                                                                                                                                                                                                          16336
Hexon protein irion component II"
                                                                                                                                                             pV protein
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                                                     associated
                                                                   protein
                                                                                                        late mRNA L2 poly-A signal (putative)"
                                                                                                                                                  core
                                                                                                                                                                                                   protein
to major core protein"
                                                                                                                                               protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residues 1-32815of Ad2'
                                                                                                                                                                                                                                                           TII"
                                                     precursor'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279
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Adeno: virus-based gene therapy vectors - esp. useful for gene therapy of cystic fibrosis

Example 15; Page 84-95; 167pp; English.

Contains a gequence represents the nucleotide sequence of the second generation adenovirus vector named Ad2-ORF6/GK-CFTR. This virus lacks El and in its place comtains a modified transcription unit with the phosphoglycerate contains a modified transcription unit with the phosphoglycerate place comtains a modified transcription unit with the phosphoglycerate contains a modified transcription of the vactor has also been modified to promoter is only if moderate strength but it is long lasting and is not contained to shut off. The E4 region of the vactor has also been modified in that the whole sequence has been removed and replace by ORF6, the construct comprises a full length copy of the Ad2 genome from the DNA construct comprises a full length copy of the Ad2 genome from the DNA construct comprises a full length copy of the Ad2 genome from the CC which the early region 1 genes (El genes) have been deleted and replaced by an expression cassette encoding CFTR. The expression cassette conducter for PGK and a poly-A addition signal from the CC includes the promoter for PGK and a poly-A addition signal directly construct the promoter of the promoter in the construct of form the construct of the promoter of the promoter in the construct of the promoter of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUN-1994.
02-DEC-1993; U11667.
03-DEC-1992; US-985478.
01-OCT-1993; US-130682.
13-OCT-1993; US-136742.
(GENZ ) GENZYME CORP.
Armentano D, Couture LA,
WPI; 94-200277/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _polya_signal
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35013.
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33081.
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/product= DBP protein
/product= "DNA binding or 72K protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= aa
/note= "pgk promoter"
1011. .5453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= E3 19K protein /note= "Glycosylated memi 1707 ... 32012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-
31051.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= 100K protein
/note= "Hexon assembled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag-
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lement (244729. .26318)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uct- E3 11.6K proteir
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.31530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "major late mRNA L5 poly-A signal (putative)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "E3-1 mRNA poly-A signal (putative)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .32013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hexon-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor'
the gene therapy of cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein"
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Query Match
Best Local Similarity
Matches 80; Conserv

Conservative

23.2%; >--100.0%; Pr

Score 80; Pred. No.

DB 1; I 6.2e-17

Length 3653

Mismatches

Indels

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ည္သင္တ
PT Recombinant adeno-associated virus contg. second gene which from the facilitates its conversion from single stranded to double stranded the facilitates its conversion from single stranded to double stranded for virus - enhances efficiency of ex vivo transduction into target cell for the stample 1; Page 69-72; 131pp; English.

Example 1; Page 69-72; 131pp; English.

This is the nucleotide sequence of a minigene containing the human cadenovirus type 5 (Ad5) E4 region open reading frame (ORF) 6 under control of the mouse mammary tumour virus promoter and a growth hormone terminator sequence. The minigene is used to generate a packaging cell line expressing the E4 ORF6 product which is used to rescue and package can E4 deficient recombinant adeno-associated virus (rAAV). The rAAV comprises at least 2 selected genes, the first gene able to express the composition gene able to convert the single stranded virus to its double stranded form upon expression. The rAAV is useful in pharmaceutical compositions for use in ex vivo and convert of the reaction of the target cell; and the second gene able to convert the single stranded virus to its double stranded form upon expression. The rAAV is useful in pharmaceutical compositions for use in ex vivo and convert cell dysfunctions, e.g. cystic fibrosis.

So sequence 3653 BP; 860 A; 851 C; 933 G; 963 T;
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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                               04-JUN-1996; U10245.
05-JUN-1995; US-462014.
27-OCT-1995; US-549489.
(UYPE-) UNIV PENNSYLVANIA.
Fisher KJ, Gao G, Wilson.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35975 ATGAAATATGACTACGTCCGGCGTTCCATTTGGCATGACACTACGACCAACACGATCTCG 35916
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minigene; human adenovirus type 5; open reading frame; promoter; in mouse mammary tumour virus; growth hormone; terminator; recombinant packaging cell line; adeno-associated virus; ex vivo; gene therapy; inherited disease; cancer; genetic dysfunction; cystic fibrosis; ds
                                                                                                                                                                                                                                                                                                 WPI; 97-043152/04.
P-PSDB; W01729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promoter
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12-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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/transl_except=
2409. .3654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product - human Ad5 E4 region ORF6 protein note - "specification gives this CDS at nuc 523-2408"
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No. 2.5e-18;
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.2093, aa:
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DE: Second generation recombinant adenoviral vector pAV.CMVALP.GRE-ORF6.

KNY-Minigener human adenovirus type 5; open reading frame; promoter; in vivo;

KNY-Minigener human adenovirus type 5; open reading frame; promoter; in vivo;

KNY-Minigener human adenovirus; growth hormone; terminator; recombinant;

KNY-TPACKAGING.Cell line; adeno-associated virus; ex vivo; gene therapy;

KNY-TPACKAGING.Cell line; adeno-associated virus; ex vivo; gene therapy;

KNY-TPACKAGING.Cell line; adeno-associated virus; ex vivo; gene therapy;
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04-JUN-1996; US-462014.
05-JUN-1995; US-54914.
27-OCT-1995; US-549489.
(UYPE-) UNIV PENNSTLVANIA.
Fisher KJ, Gao G, Wilson JM;
WPI; 97-043152/04.
Recombinant adeno-associated virus contg. second gene which facilitates its conversion from single stranded to double stranded virus - enhances efficiency of ex vivo transduction into target cell Example 19; Page 108-114; 131pp; English.

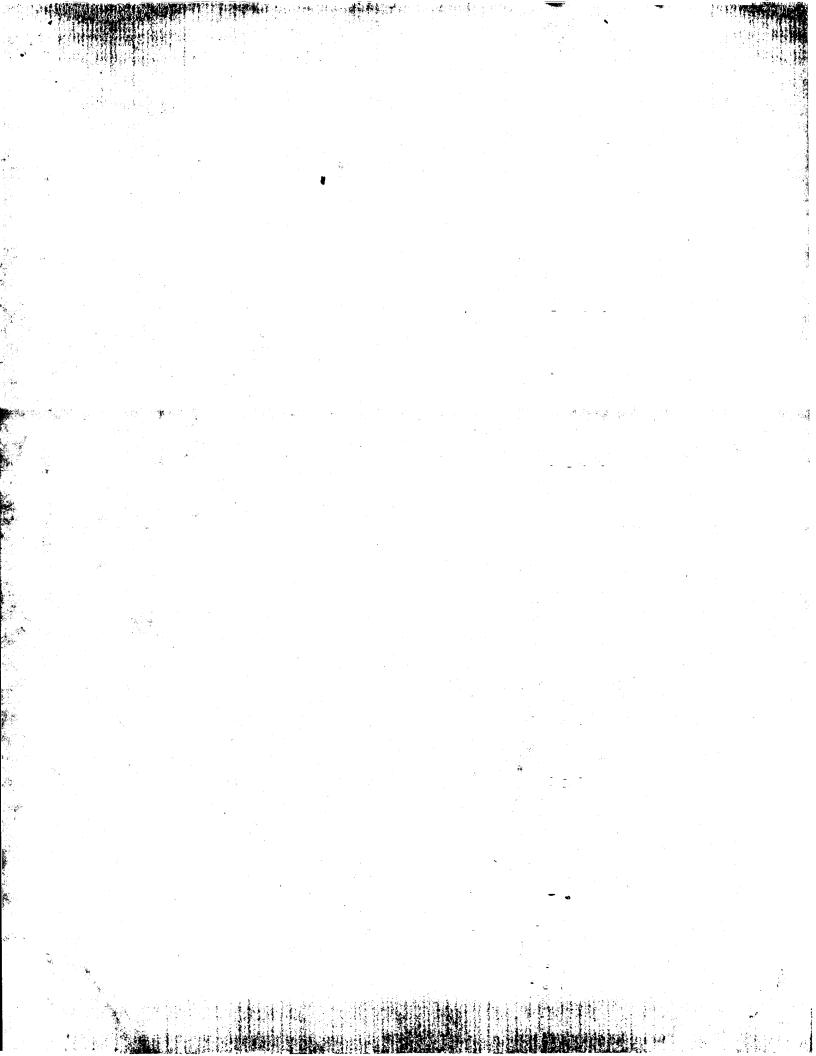
This is the nucleotide sequence of a second generation of recombinant adeno-associated virus (rAAV) which contains 2 genes, the first gene able to express the gene of interest (beta-galactosidase) in the target cell; and the second gene(AdS 24 ORF6) able to convert the single stranded virus to its double stranded form upon expression. The rAAV is useful in pharmaceutical compositions for use in ex vivo and in vivo gene therapy for the treatment of inherited diseases, cancer and other genetic dysfunctions, e.g. cystic fibrosis.

See also T59271 for amouther example of a recombinant adeno-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter
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/note= "3' AAV ITR"
4714. .8299
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4547. .4713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "plasmid derived sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product= Ad5 E4 ORF6 product
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iote= "cytomegalovirus enhancer/promoter"
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	3462 CGGC	326 cggcg	3402 ATGAC	266 atgad	ery Match st Local Si tches 80	virus. Sequence
	3462 CGGCGCACTCCGTACAGTAG 3481	326 cggcgcactccgtacagtag 345	CTACGTCCGGCG	ctacgtccggcg	lmilarity Conservat	8299 BP;
	GTAG 3481	gtag 345	3402 ATGACTACGTCCGGCGTTCCATTTGGCATGACACTACGACCAACACACGATCTCGGTTGTCT 3461	266 atgactacgtccggcgttccatttggcatgacactacgaccaacacgatctcggttgtct 325	Query Match 23.2%; Score 80; DB 1; Length 8299; Best Local Similarity 100.0%; Pred. No. 8.7e-17; Matches 80; Conservative 0; Mismatches 0; Indels	1816 A;
			ATGACACTACGA	atgacactacga	re 80; DB 1 ed. No. 8.7e Mismatches	2130 C;
			CCAACA	ccaaca	; Ler -17; 0;	2108 G;
			CGATO	logato	igth 8 Indel	<u>ن</u>
			TCGGT	tcggt:	1299; .s	1963 т;
			TGTCT	tgtct	0; Gaps	Н.
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Search completed: June 23, 2000, 10:06:58 Job time: 3686 sec



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COMMENT
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AUTHORS
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Best Local Similarity
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               JOURNAL
MEDLINE-
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Sequence 4 from Patent WO9622378.
A52460
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Other publication AU 4544396 960807
Other publication FR 2729674 960726
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Dedieu, J., Latta, M., Orsi
CELLS FOR THE PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unidentified
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                                                                                    protein 5 precursor; protein IIIa; protein V; protein pVI; protein pVII; protein pVIII.

Buman adenovirus 5 DNA.

Buman adenovirus type 5

Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

1 (bases 1 to 35935)
                       The sequence of the genome of adenovirus type 5 and its with the genome of adenovirus type 2 Virology 186 (1), 280-285 (1992)
                                                                                                                                                                                          Mastadenovirus h5 gene,
M73260 M29978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mclassified
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                                                                      Chroboczek, J., Bleber, F. and Jacrot, B.
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ilarity 100.0%;
Conservative (
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/db_xref="taxon:32644"
912 c 631 g 67
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1. .3189
Location/Qualifiers
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pnnoitslydkmsmktyaogerndvfgprpftrrokhdrokglyweddbsaddssyld
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Qiptisstsiatategmetotspyasayadaaygayaaaaskistevotdpwerrysa
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Adenovirus type 2, complete genome.

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                                                                                                                              alternative splicing; coat protein; protein; glycoprotein; overlapping ; repeat; unidentified reading frame;
                                                                 Human adenovirus type 2.
Human adenovirus type 2
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SFTPRQAILTLQTSSSEPRSGGIGTLQFIEEFVPSVYFNPFSGPPGHYPDQFIPNFDA
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Arrand, J.R. and Roberts, R. J.
The nucleotide sequences at the termini
J. Mol. Biol. 128 (4), 577-594 (1979)
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Ziff,E.B. and Evans,R.M.
Coincidence of the promoter and capped adenovirus 2 major late transcription u Cell 15 (4), 1463-1475 (1978)
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Nucleotide sequence at the junction between the coding region
the adenovirus 2 hexon messenger RNA and its leader sequence
Proc. Natl. Acad. Sci. U.S.A. 75 (12), 5822-5826 (1978)
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Pan,J., Celma,M.L. and Weissman,S.M.
Studies of low molecular weight RNA from cells 1 adenovirus 2. III. The sequence of the promoter J. Biol. Chem. 252 (24), 9047-9054 (1977)
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Studies of low molecular weight RNA from cells infected with adenovirus 2. II. Heterogeneity at the 5' end of VA-RNA I J. Biol. Chem. 252 (24), 9043-9046 (1977)
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                     protein 5 precursor; protein IIIa; protein V; prot
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Human adenovirus type 5
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae
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The sequence of the genome of adenovirus type 5 and
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Dedieu, J., Latta, M., Orsini, C., Perric CELLS FOR THE PRODUCTION OF RECOMBINAN Patent: WO 9622378-A 4 25-JUL-1996; RHONE POULENC ROKER SA (FR) Other publication AU 4544396 960807. Other publication FR 2729674 960726.
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/protein_id="AAA96407.1"
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IVQHSRDNEAFRDALLNIVEPEGRWLLDLINILGSIVVQERSLSLADKVAAINVSMLS
IGKFYARKIYHTPYVPIDKEVKIEGFYMRMALKVLTLSDDLGVYRNERIHKAVSVSRR
RELSDRELMHSLQRALAGIGSGDREAESYFDAGADLRWAPSRRALEAAGAGPGLAVAP
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ION Adenovirus type 2, complete genome.

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J01943 J01954 J01956 J01957 K00008 K00394 K00395 K02357

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J01917.1 G1:209811

DNA polymerase; DNA-binding protein; RNA polymerase III;

BNA polymerase; DNA-binding protein; complete genome; genome-linked alternative splicing; coat protein; complete genome; genome-linked protein; glycoprotein; overlapping genes; polymerase; terminal repeat; unidentified reading frame; virus-associated RNA.

Human adenovirus type 2.
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/translation="MSKEIPTDYMMSYQPQMGLAAGAAQDYSTRINYMDRDAQAEVQMT
NGIRAHRNRILLEQAAITTTPRNNLNPRSWPAALVYQESPAPTTVVLPRDAQAEVQMT
NSGAQLAGGERHRVRSPGQGITHLTIRGRGIQLNDESYSSILGLRPDGTFQIGGAGRP
SETPRQAILTLQTSSSEPRSGGIGTLQFIEEFVPSVYFNPFSGPPGHYPDQFIPNFDA
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/protein_id="AAA96413.1"
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J. Biol. Chem. 246 (22), 6991-7009 (1971)
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                                                                                                                                                                                                                                                                                                                                                                       hases 21607 to 21816)
Akusjarvi, G. and Pettersson, U.
Sequence analysis of adenovirus DNA.
carboxy-terminal end of the gene for
Virology 91 (2), 477-480 (1978)
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Zain,B.S. and Roberts,R.J.
Characterization and sequence
the hybrid virus Ad2+ND
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5an, J., Celma, M.L. and Weissman, S.M.

Studies of low molecular weight RNA from cells infected with adenovirus 2. III. The sequence of the promoter for VA-RNA I J. Biol. Chem. 252 (24), 9047-9054 (1977)
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                                                                                                                                                                                                                            Zain,S.,
Dunn,A.R.
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Ziff, E.B. and Evans, R.M.
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Nucleotide sequence at the junction between the coding region
the adenovirus 2 hexon messenger RNA and its leader sequence
proc. Natl. Acad. Sci. U.S.A. 75 (12), 5822-5826 (1978)
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                                                                                                                                                               Nucleotide sequence analysis of copy of adenovirus 2 fiber mrNA Cell 16 (4), 851-861 (1979), 79211249
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Lysis of adenovirus DNA:
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Human adenovirus type 5

Viruses; dabNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

Viruses; dabNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

Viruses; dabNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

Chooboczek, J., Bieber, F. and Jacrot, B.

The sequence of the genome of adenovirus type 5 and its comparison roughly genome of adenovirus type 2

Virology 186 (1), 280-285 (1992)
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M73260 M29978
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pvII; protein pvIII.
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relsdrelmhsloralagigsgdreaesyfdagadlkwapsrraleaagagpglayap
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RDGVTPSVALDNTARNNEPGMYASNRPFINRLMDYLHRAAAVNPEYFTNAILNPHNLD
RDGVTPSVALDNTARNNEPGMYASNRPFINRLMDYLHRAAAVNPEXFATALRESFRRPSS
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PNNGIESLVDKNSRWKTYAQEHRDVPGPRPPTRRQRHDRQRGLVWEDDDSADDSSYLD
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TTRPIAPMATGVLGQUGTUTLDLPPPADTQQKFVLPGPTAVVVTRPSRASLRRAASGP
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DGRLGEPRRGSFRGRRGVRRNTVTLGRIPLAGAPEIGNRFQHGYNLRSSGAAGTARSP
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KEYWORDS
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Akusjarvi,G. and Pettersson,U.
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Carboxy-terminal end of the gene for
Virology 91 (2), 477-480 (1978)
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Nucleotide sequence at the junction between the coding region
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Zain,B.S. and Roberts,R.J.
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the hybrid virus Ad2+ND
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The nucleotide sequence of a low molecular from cells infected with adenovirus 2
J. Biol. Chem. 246 (22), 6991-7009 (1971)
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d N-terminus of adenovirus type 2 hexon protein
phys. Res. Commun. 56 (2), 304-310 (1974)
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SUMMARIES

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glucosylceramidase complement C5a ana NADH dehydrogenase

ABC transporter phospholipase C NADH dehydrogenase

ALIGNMENTS

R;Herisse, J.; Rigolet, M.; Dupont de Dinechin, S.; Galibert, F. Nucleic Acids Res. 9, 4023-4042, 1981
A;Title: Nucleotide sequence of adenovirus 2 DNA fragment encoding A;Reference number: A93733; MUID:82059444
A;Accession: A03805 early E4 34K protein - human adenovirus 2
()Species: Mastadenovirus h2 (human adenovirus 2)
A;Note: host Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 04-Mar-1994
C;Accession: A03805 A;Map position: 92.6-95.2 C;Superfamily: adenovirus early E4 34K protein C;Keywords: early protein A; Note: this probable protein was assigned by correlating C; Genetics: A; Molecule type: DNA A; Residues: 1-294 <HER> EM data and Si digestion for the carboxylic

Query Match 100.0%; Score 1594; DB 1; Length 294; Best Local Similarity 100.0%; Pred. No. 9.3e-142; Best Local Similarity 100.0%; Pred. No. 9.3e-142; Best Local Similarity 100.0%; Pred. No. 9.3e-142; Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0 1 MITSGVPFGMTLRPTRSRLSRRTPYSRDRLPPETETRATILEDHPLLPECUTLIMHNVS 60 1 MITSGVPFGMTLRPTRSRLSRRTPYSRDMLPFETETRATILEDHPLLPECUTLIMHNVS 60 1 MITSGVPFGMTLRPTRSRLSRRTPYSRDMTHQLFTWREVVNYNMPKEVMFMSSWF 120 61 YVRGLPCSVGFTLIQEMVVPMDMVLTREELVILRKCMHVCLCCANIDIMTSMMIHGYESW 120 61 YVRGLPCSVGFTLIQEMVVPMDMVLTREELVILRKCMHVCLCCANIDIMTSMMIHGYESW 120 9 121 ALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFTWRREVNYNMPKEVMFMSSVF 180 121 ALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFTWYREVNYNMPKEVMFMSSVF 180 122 ALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFTWYREVNYNMPKEVMFMSSVF 180 123 ALHCHCSSPGSLQCIAGGQVLASWFRMVVDGAMFNQRFTWYREVNYNMPKEVMFMSSVF 180 124 MTRRLMLRAVENJAGETTAMLYSCRTERRRQQFTRALLQHHRPILMHDYDSTPM 294 181 MGRHLIVLHILLIHILLIHIHIHIHIHIHIHIHIHIHIHIHIH
100.0%; Score 1594; DB 1; Length 294; Similarity 100.0%; Pred. NO. 9.3e-142; 4; Conservative 0; Mismatches 0; Indels 0; Ga 4; Conservative 0; Mismatches 0; Ga 6; Mismatches 1; Mismatches 0; Ga 6; Mismatches 1; Mismatches 1; Mismatches 0; Ga 6; Mismatches 1; Mismatches 1; Mismatches 0; Ga 6; Mismatches 1; Mism
Length 294; Indels 0; GB HPLLPECNTLTMHNVS
ps 0 60 60 1120 1120 1180 1180 240

RESULT S10867

early E4 34K protein - human adenovirus 12 c;Species: Mastadenovirus hi2 (human adenovirus 12) c;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999 c;Accession: S10867; S33952 R;Hogenkamp, T.; Esche, H.

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